

STIC Database Tracking Number

TO: Cynthia Wilder Location: Rem 2a35

Thursday, February 12, 2004

Art Unit: 1637 Phone: 272-0791

Serial Number: 09 / 981606

From: Jan Delaval

Location: Biotech-Chem Library

Rem 1A51

Phone: 272-2504

jan.delaval@uspto.gov

Search Notes



STIC-Biotech/ChemLib

13949

From:

Chan, Christina

Sent:

Tuesday, February 10, 2004 9:23 AM Wilder, Cynthia, STIC-Biotech/ChemLib

To: Subject:

RE: Rush sequence search for 09/981606

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841Remsen, 3E89

----Original Message----

From:

Wilder, Cynthia

Sent:

Tuesday, February 10, 2004 9:09 AM

To:

Chan, Christina

Subject:

Rush sequence search for 09/981606

Ms. Chan,

I am requesting a rush sequence search and for interference of the following: 09981606. This case needs prompt attention.

Please forward your approval to STIC

Please provide a search of nucleotides 67-339 of SEQ ID NO: 1, wherein at position 193 and A is substituted for a T.

Please provide a search of nucleotides 700-850 of SEQ ID NO: 1, wherein a mutation is located at nucleotide 845.

Please provide a search of nucleotides 4652-4915 and nucleotides 6494-6927 of SEQ ID NO: 27.

Thank you

Cynthia B. Wilder, Ph. D. United States Patent and Trade Mark Office Carlyle Remson 2035 2018 (571) 272-0791

Searcher:	2250	
Location: Date Picked Up: Date Completed:	2112	- 11/2 de 1
Searcher Prep/Revie Clerical: Online time:	ew: _10 _720_	* X.V. \

TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: www/Internet: Other (specify):

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replace(408, "c")
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LOCATION: replace
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LOCATION:
FEATURE:
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                                                                         February 11, 2004, 15:39:52; Search time 49.5778 Seconds
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US-08-834-497A-9
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US-09-503-444A-9
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Maximum Match 100%
Listing first 45 summaries
                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: Thomas, Winstom J.
APPLICANT: Thomas, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Grirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchinashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Zenta
APPLICANT: Touchihashi, Zenta
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENT Release #1.0, Version #1.30

SUFTWARE: PATENT Release #1.0, Version #1.30

GURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION NUMBER: 31,23

REFERENCE/ORGET INFORMATION:

NEGLISTATION NUMBER: 17957-000500

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FOR EQUID NO: 9:

SEQUENCE CHRACTERISTICS:

LENGTH: 1440 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MULECULE TYPE: CDNA
US-08-834-497A-5
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US-09-16-077-7
US-08-890-719-5
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US-08-774-025A-4
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US-08-774-025A-4
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                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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        10825
10825
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           259.8
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
FEATURE:
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99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Gairke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
/phenotype= "normal or wild-type (unaffected)" /label= 2442
                                                                                                         "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STREE: California COUNTRY: USA
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                                                                                                         /phenotype= "nc
(unaffected)"
/label= 24d7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08652265 Parent No. 6025130 GENERAL INFORMATION:
                                                                           NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
                                                                                                                                                                             NAME/KEY: allele
LOCATION: replace(1066, "g")
COTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
US-08-652-265-9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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        OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OP INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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99.4%; Score 271.4; DB 3;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1;
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/08834497A; Patent No. 6140305
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: New York
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NAME/KEY: allele
CACATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, winston J.
APPLICANT: Thomas, winston J.
APPLICANT: Breder, John N.
APPLICANT: Grirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: 04-APR-1997
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: US 08/630,912
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T: 1155 Avenue of the Americas
New York
: New York
                                                                                                                                                                                                                                                          Sequence 10, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222..1268
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10036-2811
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                                                                                                                                                                                                                                           US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /phenotype= "normal or wild-type (unaffected)" / label= 24d2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /phenotype= "normal or wild-type (unaffected)"
               OPERATING SYSTEM: Windowe 95
SOGTWARE: FeatSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 33-MAY-1996
CLASSIFICATION DATA:
APPLICATION S14
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
ATTORNEY/AGENT UNFORMATION:
NAME: POISSANT, BIAN M.
REGISTRENCY INFORMATION:
NAME: POISSANT, BIAN M.
REGISTRENCY OCKET VINBER: 8907-0056-999
TELEPRAN: 660-493-4935
TELEPAX: 66141 PENNIE
TELEPAX: 66141 PENNIE
TELEX: 66141 PENNIE
TENNICH: 1440 base pairs
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; LOCATION: replace(1066, "g")
; OTHER INFORMATION: /phenotype;
; OTHER INFORMATION: (unaffecte;
; OTHER INFORMATION: /label= 24
US-08-834-497A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace (414, "a")
OTHER INFORMATION: /phenoty
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label=
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OTHER INFORMATION: /phenoty
OTHER INFORMATION: (unaffec
OTHER INFORMATION: /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: allele
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APPLICANT: Thomas, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF TRUCHING: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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LOCATION: replace(1066, "g")
OTHER INFORMATION: (phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /phenotype= "normal or wild-type (unaffected)" / label= 2442
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(unaffected)"
/label= 24d7
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Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennie & Edmonds LLP
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OTHER INFORMATION: /phenoty
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OTHER INFORMATION: /phent
OTHER INFORMATION: (unaff
OTHER INFORMATION: /label
FEATURE:
NAME/KEY: allele
                              TELEX: 66141
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FRATURE:
212-869-9741
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
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      TELEFAX:
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                                                                                                                                                                                                                                                                            61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 GGICTTICCTIGITICAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407
                                                                                                                                                                                                                                    1 CGCTTGCTTGCGACTCTTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                           ;
0
                                                                                                    Query Match

99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09503444A
; Sequence 9, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
    APPLICANT: Thomas, Winston J.
    APPLICANT: Feder, John N.
    APPLICANT: Gnirke, Andreas
    APPLICANT: Freder, John N.
    APPLICANT: Wolff, Andreas
    APPLICANT: Wolff, Roger K.
    ITLE OF INVENTION: Hereditary Hemochromatosis Gene
    NUMBER OF SEQUENCES: 44
    CORRESPONDENCE ADDRESS: CORRESPONDENCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 regacratraregaaarcacaaccacadae 560
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REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 8907-0088-999
TELECOMUNICATION INFORMATION:
TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordbriect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY AGENT INFORMATION:
                ; OTHER INFORMATION: /label= 24dl
US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
ZIP: 10036
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US-09-503-444A-9
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181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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Sequence 1, Application US/09679729

Sequence 1, Application US/09679729

FAREAR NO. 6509442:

APPLICANT: Rothenberg, Barry E.

APPLICANT: Barton, James C.

ITILE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS

FILE REFERENCE: 24065-004 DIV

CURRENT PAPLICATION NUMBER: US/09/679,729

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2506

TYPE: DNA

CORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 271.4; DB 4; Length 2506;
Pred. No. 6e-82;
0; Mismatches 1; Indels 0;
                              US-09-277-457-1
; Sequence I, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rotherherig, Barry E.
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MOTHATIONS ASSOCIATED WITH IRON DISORDERS FILE REPERRECE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277.457
; UURBER OF SEQ ID NOW: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (0)...(0); OTHER INFORMATION: Missense mutation at nucleotide 314 US-09-277-457-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 TGGACTATTATGGAAATCACAACCACAGCAAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
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NAME/KEY: mutation
LOCATION: (0) ...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mutation
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 2506
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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99.4%; Score 271.4; DB 3; Length 1440;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype= "Hereditary Hemochromatosis
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WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Worderfect Version
SOFTWARE: Worderfect Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 25-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 16-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISBEAT INFORMATION:
NAME: POISBEAT INFORMATION:
REFERENCE/DOCKET NUMBER: 89.07-0088-999
TELEFRAN: 212-869-9741
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 222..1268
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                     New York
: New York
RY: USA
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                                            STATE: Ne
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Gaps

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222..1268
NAME/KEY: CDS
LOCATION: 222..126
FEATURE:
NAME/KEY: allele
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US-08-652-265-12
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                                                                                                                                             1 CGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                        Gaps
                                                                                                      0;
                                                            Length 2506;
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APPLICANT: Thomas
APPLICANT: Dennis
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Hauchinhash;
APPLICANT: Herchitash;
APPLICANT: Herchitash;
APPLICANT: Herchitash;
APPLICANT: Herchitary Hemochromatosis Gene
                                                            Score 271.4; DB 4; Length 2
Pred. No. 6e-82;
0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
  ; OTHER INFORMATION: Missense mutation at nucleotide 314 US-09-679-729-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
California
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6025130
GENERAL INFORMATION:
                                                                 99.4%;
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                                                               Query Match
Best Local Similarity 99.6
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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FEATURE:
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98.8%; Score 269.8; DB 3; Length 1440;
Best Local Similarity 99.3%; Pred. No. 1.6e-81;
Matches 271; Conservative 0; Mismatches 2; Indels 0;
| LOCATION: replace(408, "q") | COMPATION: replace(408, "q") | OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2 | OTHER INFORMATION: /label= 24d2 | US-08-652-265-11
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION F76-0300
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayra, Dennis T.
APPLICANT: Golike, Andreas
APPLICANT: Golike, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Pubarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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Patent No. 6025130
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FastSEQ for Windows Version 2.0b
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LOCATION:
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US-08-834-497A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CATGAGTGTCGCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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Local Similarity 99.3%; Pred. No. 1.6e-81;
Los 271; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                    /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "Hereditary Hemochromatosis
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08834497A, Patent No. 6140306 GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                      /label= 24d1
                                                                                                                                                                                                                                                                                               /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY I
                                                                                                                                                                                                                                                                                                                                                     JOCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
US-08-652-265-12
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                LOCATION: replace (408, "g")
OTHER INFORMATION: /phenotyn
OTHER INFORMATION:
OTHER INFORMATION: /label=
                         LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                     CDS
222..1268
                                                                                                                                                                                                                 NAME/KEY: allele
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                                                                                          linear
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ZIP: 10036-2811
                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                     NAME/KEY:
LOCATION:
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Matches
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121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMES/KEY: allele
LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: /label= 24d2
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 269.8; DB 3; Length Pred. No. 1.6e-81; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8907-0056-999
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 23-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION STA
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION STA
ATTORNEY/AGENT INFORMATION:
NAME: POISSART, BIAID M.
REGISTRATION NUMBER: 89.462
RESERENCE/DOCKET NUMBER: 89.07-0056-9
TELECOMMUNICATION NUMBER: 89.07-0056-9
TELECOMMUNICATION NUMBER: 89.462
     од-држ: US/08/834,497A
04-дрк-1997
V:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.8%;
Best Local Similarity 99.3%;
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
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181 AIGIGGCIGCAGCIGAGICAGAGICTGAAAGGGIGGGAICACAIGIICACIGIIGACTIC 240
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                                                                                                                     121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                   468 AIGIGGCIGCAGCIGAGICAGAGICAGAGGIGGGAICACAIGTICACIGITIGACITIC 527
CGCTTGCTGCGCTTCACACTCTTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 60
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-503-444A-11
) Sequence 11, Application US/09503444A
) Patent No. 6228594
) GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Ruddy, David Senta
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
CORRESPONDENCES: Appune & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
SIPP: 1155
                                                                                                                                                                                                                                                                                                                                                        TGGACTATTATGGAAAATCACAACCACAGGAAG 273
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SUCTRARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION: 14-Feb-2000
CLASSIFICATION: APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
PRICA PAPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRICA APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
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INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace (1066, "a")
CTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
US-08-834-497A-12
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                                                                         APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                        STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compartible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
FILING DATE: 04-APR-1996
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POISBART, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(408, "g")
         Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
NAME/KEY: allele
LOCATION: replace (408
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EDNESS: single
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Best Local Similarity
Matches 271; Conserva
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NAME/KEY: allele
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           APPLICANT:
APPLICANT:
APPLICANT:
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US-09-503-444A-12
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                               Length 1440;
                                                                                                                                             LOCATION: replace(408, "g")

TOTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                        Indels
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                           Query Match 98.8%; Score 269.8; DB 3 Best Local Similarity 99.3%; Pred. No. 1.6e-81; Matches 271; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 528 TGGACTATTATGGAAAATCACAACCACAGGAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09503444A Patent No: 6228594
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                               CDS
222..1268
                  MOLECULE TYPE: CDNA
                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-503-444A-12
                                                             NAME/KEY:
LOCATION:
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TOPOLOGY:
                                           FEATURE:
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288 electricericacaerereceaeracerereares 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 GGTCTTTCCTTGTTTGAAGCTTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407
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LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24di
OTHER INFORMATION: /label= 24di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 269.8; DB 3; Length
Pred. No. 1.6e-81;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 regacrarraregaaaarcacaaccacaac 560
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                                                                                                      08/630,912
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FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,91
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INPORMATION:
NAME: POISSAIL, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
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Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.8%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 222..1268
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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Best Local Similarity
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APPLICANT: Thomas,
APPLICANT: Peder, U
APPLICANT: Reder, APPLICANT: Ruddy, D
APPLICANT: Ruddy, D
APPLICANT: Ruddy, D
APPLICANT: Wollf, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6025130mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: Allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allale (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)" (SEQ ID NO:9)" NAME/KEY: - LOCATION: 3852.3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /phenotype= "normal or wild-type (unaffected)" /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "normal or wild-type (unaffected)" /label= 24d7
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-LOUS, MNS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, William M.
REGISTRATION NUMBER: 17957-000500
TELEPAATION NUMBER: 17957-000500
TELEPAATION NUMBER: 17957-000500
TELEPAATION INFORMATION:
TELEPAONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS:
                                                                           E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION: (unaffect
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= ct
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NAME/KEY: -
LOCATION: 140..7319
                                                                                                                        CITY: San Francisco
STATE: California
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                                                                             ADDRESSEE:
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3942 AGCTGAGTCTGAAGGTGGAAGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
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                                                                                                                                                                                                                                                                                                                            71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 130
                                                                                                                                                                                                                                                        3762 GITCACACTCICTACACACTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                   131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                    11 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                0; Gaps
                                                                                                                                        Length 10825;
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Query Match
95.8%; Score 261.4; DB 3;
Best Local Similarity 99.6%; Pred. No. 2.8e-78;
Matches 262; Conservative 0; Mismatches 1;
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ne : 51.5778 secs
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Sequence 487, Application US/60487610
                                                     TYPE: JNA
ORGANISM: Homo sapiens
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US-60-487-610-487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 485,
                                                                                                                                                                                                                                                                                                                                            1 cgcttgctgcgttcacactc.....aaaatcacaaccacagcaag 273
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

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6: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USIO_NEW_COMB.seq:*
5.1.6
Compugen Ltd.
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US-60-524-882-107
US-60-487-610-19486
PCT-USO3-40978-17631
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US-60-487-610-487
US-60-487-610-487
US-10-741-600-272
US-10-741-600-272
US-10-741-600-266
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US-10-741-600-266
US-10-741-600-271
US-10-741-600-271
US-10-741-600-271
US-10-741-600-271
US-10-741-600-261
US-10-741-600-261
US-60-524-882-111
PCT-US03-40978-267
US-60-524-882-1104
PCT-US03-40978-267
US-60-524-882-109
PCT-US03-40978-267
US-60-524-882-109
PCT-US03-40978-267
US-60-524-882-109
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  GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                 nucleic search, using
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seq length: 200000000
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TITLE OF INVENTION:
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                                   9114, Ap
262, App
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103, App
1103, Ap
7447, Ap
7525, Ap
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US-10-741-600-17631

US-60-54-882-9174

US-60-482-9174

US-60-482-1074

US-10-741-600-262

US-10-741-600-262

US-60-524-882-1033

PCT-US03-40978-7447

PCT-US03-40978-7447

PCT-US03-40978-7462

PCT-US03-40978-7462

PCT-US03-40978-7525

PCT-US03-40978-7549

PCT-US03-40978-7549

PCT-US03-40978-7549

US-10-741-600-7362

US-10-741-600-7462

US-10-741-600-7462

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US-10-741-600-7462
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Best Local Similarity 98.2
Matches 268; Conservative
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT PEPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PASLSEQ for Windows Version 4.0
LENGTH: 746
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GENERAL INFORMATION:
APPLICANT: CARGILL,
APPLICANT: CARGILL,
APPLICANT: APPLICANTON:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERRENCE: CLO01494
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT PILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SOGTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 746
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                                                                            181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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  181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
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Pred. No. 2.2e-84;
8; Mismatches 0;
                                                                                                                                                                          241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                      528 TGGACTATTATGGAAAATCACAACCACAGGAAG 560
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ilarity 97.1%;
Conservative
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; ORGANISM: Homo sapiens
US-10-741-600-272
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ORGANISM: Homo sapiens
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US-60-524-882-114
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001499
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HERATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: LIVER FIBROSIS IN HERATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: MITHOUS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01469
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTHARE: FASTERE for Windows Version 4.0
ENGTHARE: 2285
LENGTH: 2285
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Pred. No. 2.2e-84;
8; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 271; DB 8; Length 2285; Pred. No. 1.3e-84; 5; Mismatches 0; Indels
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CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 272
LENGTH: 746
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97.1%;
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Best Local Similarity 98.2%;
Matches 268; Conservative
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Matches 265; Conservative
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PCT-US03-40978-272
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US-60-487-610-487
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, ORGANISM: Homo sapiens
US-10-741-600-266
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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LENGTH: 2009
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 266
LENGTH: 2009
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Pred. No. 3.3e-84;
8; Mismatches 0;
                                  DB 8;
                                98.8%; Score 269.8; DB 8 97.1%; Pred. No. 2.2e-84; iive 8; Mismatches 0
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Best Local Similarity 97.1%;
Matches 265; Conservative
                                   Query Match 98.8
Best Local Similarity 97.1
Matches 265; Conservative
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US-10-741-600-266
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REPERBUCE: CLOOL499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILIAG DATE: 2003-12-22
SUFFMENT FILIAG DATE: 2003-12-22
SUFFMENT FILE SECTION NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1494
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT APPLICATION NUMBER: US/60/524,882
SUFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 3.3e-84;
8; Mismatches 0; Indels 0;
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Best Local Similarity 97.1%;
Matches 265; Conservative
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Sequence 113, Application US/60524882
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDITOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT APPLICATION NUMBER: US/60/524,882
CURRENT FILING DATE: 2003-11-26
SURPHARE: FASESQ ID NOS: 46672
SEQ ID NO: 46672
SEQ ID NO: 13
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Query Match 98.8%; Score 269.8; DB 6; Best Local Similarity 97.1%; Pred. No. 3.5e-84; Matches 265; Conservative 8; Mismatches 0;
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PCT-US03-40978-270
; Sequence 270, Application PC/TUS0340978
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; ORGANISM: Homo sapiens
US-60-524-882-113
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US-60-524-882-113
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73397
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT PELLING NUMBER: PCT/US03/40978
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 271
LENGTH: 2285
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SAYGAGWGTGGCCGTGTGGAGCCCYGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
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Pred. No. 3.5e-84;
8; Mismatches 0; Indels 0;
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Best Local Similarity 97.1%;
Matches 265; Conservative 8
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CORGANISM: Homo sapiens
US-10-741-600-271
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ORGANISM: Homo sapiens
PCT-US03-40978-271
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US-10-741-600-271
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001494
CURRENT FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 46672
SOFTWARE: PARLSEQ for Windows Version 4.0
SEQ ID NO 111
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Pred. No. 3.5e-84;
8; Mismatches 0;
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                                                                                                                               241 IGGACTATTATGGAAAATCACAACCACAGCAAG 273
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APPLICANT: CARGILL, Michele
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Best Local Similarity 97.1%;
Matches 265; Conservative
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; ORGANISM: Homo sapiens
US-60-524-382-111
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LENGTH: 2440
TYPE: DNA
ORGANISM: Homo sapiens
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US-60-524-882-111
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US-10-741-600-270

US-10-741-600-270

Sequence 270, Application US/10741600

GENERAL INPORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE PEPERENCE: 2003-12-22

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: PASESEQ for Windows Version 4.0

LENGTH: 2398
                                         FENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 3.5e-84;
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS TITLE OF INVENTION: MYOCARDIAL INFARCTION, M FILE REFERENCE: CLOO1499 CURRENT APPLICATION NUMBER: PCT/US03/40978 CURRENT FILING DATE: 2003-12-22 NUMBER OF SEQ ID NOS: 73997 SOFTWARE: FESTSEQ for Windows Version 4.0 SEQ ID NO 270 LENGTH: 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.8%; Score 269.8;
97.1%; Pred. No. 3.5
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Best Local Similarity 97.1
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 97.1
Matches 265; Conservative
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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US-10-741-600-270
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                                                                                                                                                                              121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                          1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTTCATGGGTGCCTCAGAGCAGGACCTT
                               0; Gaps
Query Match 98.8%; Score 269.8; DB 1; Length 2440; Best Local Similarity 97.1%; Pred. No. 3.6e-84; Matches 265; Conservative 8; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                      241 TGGACTATTATGGAAATCACAACCACAGCAAG 273
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Search completed: February 11, 2004, 22:00:54 Job time: 288.165 secs

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(c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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273
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Maximum DB seq length: 200000000
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Perfect score:
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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 77, Appl	Sequence 6940, Ap	Sequence 9, Appli	Sequence 10, Appl
ព	1440 46 US-10-138-888-77	US-60-278-232-6940	US-08-834-497-9	US-08-834-497-10
1 38	46	82	13	13
Query Match Length DB	1440	1045	1440	1440
Query Match	100.0	99.4	99.4	4.66
Score	273	271.4	271.4	271.4
Result No.	-	7	٣	4

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Sequence 6940, Application US/60278232
GENERAL INFORMATION:
APPLICANT: Moorie, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorleotide Sequence Databases, and Single Nucleotide
FILE REFERENCE: GX-0011 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: replace(414, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-76;
Matches 273; Conservative 0; Mismatches 0; Indels 0;
                                                         PILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REFERENCE/DOCKET NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89,07-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 regactartaregaaaarcacaacacacaas 560
          CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FILING DATE: 02-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
222..1268
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                                                                                                         Sequence 18074, A Sequence 18074, A Sequence 18074, A Sequence 1806, Appl Sequence 1, Appl Sequence 18068, A Sequence 18068, A Sequence 18073, A Sequence 18073, A Sequence 3472, Ap Sequence 1579, Ap Sequence 3472, Ap Sequence 3472, Ap Sequence 3474, Ap Sequence 3474, Ap Sequence 1581, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
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Sequence 11, Appl
Sequence 12, Appl
Sequence 11, Appl
                                                             Sequence 26715, A
Sequence 27072, A
Sequence 1, Appli
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GENERAL INFORMA
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Sequence 41388, .
                                               Sequence
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CORRESPONDENCE: 79
CORRESPONDENCE: 79
CORRESPONDENCE: 79
CORRESPONDENCE: 79
CORRESPONDENCE: 79
CITY: New York
COUNTRY: USA
CITY: New York
COUNTRY: USA
CIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO: DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
      US-09-497-957-10
US-10-138-88-9
US-10-138-88-9
US-10-170-235-26715
US-10-170-235-26715
US-09-981-66-1
US-09-981-66-1
US-09-724-676A-18074
US-09-949-016-1180
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US-09-724-676-18068
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US-60-453-050-3472

US-60-453-050-3472

US-60-465-241-1579

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US-60-453-050-3474

US-60-453-050-3474

US-60-453-135-3474

US-60-465-241-1581

US-60-465-241-1581

US-60-466-241-1581

US-60-466-241-1581

US-60-469-1581

US-09-915-738-1161

US-09-919-116-1181
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US-09-724-676A-18073
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US-09-949-016-41388
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APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77, Application US/10138888
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Ghiffe, Andreas
Ruddy, David
Tsuchihashi, Zenta
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RESULT 4
US-08-834-497-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AIGIGGCTGCAGCTGAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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                                                                                                                                                                                                                                                                                                              DB 82; Length 1045;
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                                                                                                                                                                                                                                                                                                                                                          1; Indels
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADBRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                            99.4%; Score 271.4; DB 8; 99.6%; Pred. No. 2.3e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                        FEATURE:
NAME/KBY: misc_feature
OTHER 1NFORMATION: Incyte ID No: 333732.1
CURRENT APPLICATION NUMBER: US/60/278,232
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 12,557
SOFTWARE: PERL Program
SEQ ID NO 6940
LENGTH: 1045
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MA-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WIMBER: US 08/632,673
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08834497
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6
Matches 272; Conservative
                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-834-497-9
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61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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PRATURE:

NAME/KEY: allele

LOCATION: replace(1066, "g")

OTHER INFORMATION: (unaffected) "

OTHER INFORMATION: (label= 24d)

OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /phenotype= "normal or wild-type
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Pred. No. 2.6e-75;
                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitch Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TERGTH: 1140 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATR:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (unaffected) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 222..1268
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
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121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                            468 ATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527
                                                   408 cardadadrodecedreredadececedaacrocardegerrocagradaarrroaagecag 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                       528 regacrarraregaaarcacaaccacagcaag 560
                                                                                                                                                                                             241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FESTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REBERENCE, POCKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEPRAN: 650-493-5556
TELEPRA: 661-41 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/634,497
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION DATE: US 08/630,912
FILING DATE: US 08/630,912
FILING DATE: US 08/630,912
FILING DATE: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                     3-09-497-957-9
Sequence 9, Application US/09497957
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Peder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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LOCATION: 222..126
FEATURE:
NAME/KEY: allele
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MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 GGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 94111-3834

COMPUTER READALE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
                                                                                                                                                 Hereditary Hemochromatosis Gene 76
PRIOR APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: FILLS, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION SECTION 18FORMATION:
TELEPHONE: (650) 326-2402
INFORMATION FOR SEQ ID NO: 10: SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype=
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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LOCATION: 222..1268
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Best Local Similarity 99.6
Matches 272; Conservative
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LOCATION: 222..1268
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CATGAGTGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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99.4%; Score 271.4; DB 21; Length 1440;
Best Local Similarity 99.6%; Pred. No. 2.6e-75;
Matches 272; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, Winston J.
APPLICANT: Tromas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Nolff, Roger K.
APPLICANT: Nolff, Roger K.
APPLICANT: TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    /phenotype= "normal or wild-type (unaffected)" /label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /phenotype= "normal or wild-type (unaffected)"
/label= 24d1
                                        "normal or wild-type
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                    /phenotype= "n.
(unaffected) "
/label= 24d2
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                                                                             OTHER INFORMATION: (unaffected OTHER INFORMATION: /label= 24 FRATURE: NAME/KEY: allele LOCATION: replace(414, "a") OTHER INFORMATION: (unaffected OTHER INFORMATION: (unaffected OTHER INFORMATION: /label= 24 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
CCATION: replace(1066, "g")
CTHER INFORMATION: /phenotype
CTHER INFORMATION: (unaffecte)
CTHER INFORMATION: /label= 24
US-09-497-957-9
replace(408, "c")
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PRIOR APPLICATION DATA:
                                    INFORMATION:
INFORMATION:
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LOCATION:
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61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGGATCACATGTTCACTGTTGACTTC 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
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Drayna, Dennis T.
Frader, John N.
Gnirke, Andreas
Ruddy, David
Teuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 regacrarraregaaaarcacaacaacaag 560
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APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 16-APR-1996
FILING DATE: 10-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSAIT, BRIAN M.
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-10-138-888-9
; Sequence 9, Application US/10138888
; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCTATGAT 407
                                                                       121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                    ATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIR Release #1.0, Version #1.30
CURRENT APPLICATION DURBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                       528 TGGACTATTATGGAAAATCACAAACCACAAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCXET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                      241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-May-2002
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATE: 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-10-138-888-10
; Sequence 10, Application US/10138888
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
222..1268
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STRANDEDNESS: single
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ZIP: 10036-2711
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: replace(414, "a")
OCHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
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LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /phenotype= "normal or wild-type
                                                                                                                              COUNTY: NAM YORK
COMPUTER: NAM YORK
COMPUTER: USA
COMPUTER: FLOPPY disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION ON THE US WAS APPLICATION DATE: PRIOR PRIOR DATE: 04-APR-1997
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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OTHER INFORMATION: /phe
(unaffected)"
/label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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LOCATION: 222..1268
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           NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 272; Conservative
                                                                                             CITY: New York
STATE: New York
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NAME/KEY:

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Sequence 27072, Application US/10170235
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSCRIPTS, 5UCH AS NUCLEIC ACID ARRAYS, COMPRISING A.MAJORITY OF HUMAN:
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
CURRENT APPLICATION UNDER: 2003-03-17
CURRENT APPLICATION UNDER: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 ATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 47; Length 2285;
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GENERAL INFORMATION:
APPLICANT: Rothenberg et al.
TILE OF INVENTION: Mutations associated with iron disorders;
FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Pred. No. 3.1e-75;
0; Mismatches 1; Indels
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Best Local Similarity 99.69
Matches 272; Conservative
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Best Local Similarity
                        RESULT. 10
US-10-170-235-27072
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ORGANISM: HUMAN
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                                                                                                                                                                                                                                                                                                               SEQ ID NO 27072
                                                                                                                                                                                                                                                                                                                                           LENGTH: 2285
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US-09-981-606-1
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: RITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF FILE REPERENCE: CLO01380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT APPLICATION NUMBER: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 26715
LIENGTH: 1724
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LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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                                                                                                                                                                                 DB 46; Length 1440;
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                                                                                                                                                                            Query Match 99.4%; Score 271.4; DB 46; Length Best Local Similarity 99.6%; Pred. No. 2.6e-75; Matches 272; Conservative 0; Mismatches 1; Indels
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99.4%; Score 271.4; DB 47; Length
Best Local Similarity 99.6%; Pred. No. 2.8e-75;
Matches 272; Conservative 0; Mismatches 1; Indels
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                                                                       /label= 24dl
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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US-10-170-235-26715
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US-10-170-235-26715
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TYPE: DNA ORGANISM: Human
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US-09-949-016-1180
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                                                          187 CATGAGAGTCGCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
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                                                                                                                                    181 ATGTGGCTGCAGCTGAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18074, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129481.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE Patentin version 3.2
SEQ ID NO 18074
                                                                                                                                                                                                                                                                           241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                       307 TGGACTATTATGGAAAATCACAACCACAGCAAG 339
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Best Local Similarity 99.6
Matches 272; Conservative
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US-09-724-676A-18074
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US-09-724-676-18074
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Sequence 1180. Application US/09949016

GENERAL INFORMATION:
THE INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOU3307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2007012
SOFTWARE: PESESEE for Windows Version 4.0
SEQ ID NO 1180
LENGTH: 2777
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Score 271.4; DB 32; Length 2619;
Pred. No. 3.3e-75;
0; Mismatches 1; Indels 0;
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      99.4%;
   Query Match
Best Local Similarity 99.6
Matches 272; Conservative
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Best Local Similarity 99.6
Matches 272; Conservative
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Sequence 64, Application US/09949016

Sequence 64, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PEASESEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 2727
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Best Local Similarity 99.68
Matches 272, Conservative
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; ORGANISM: Human
US-09-949-016-64
RESULT 15
US-09-949-016-64
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Run on:

Sequence:

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Searched:

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ACCESSION
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/db_xref="G1:11094313"
/tb_xref="G1:11094313"
/tb_xref="G1:11094313"
/tb_xref="G1:100="G1:11094313"
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562-878de1
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1 (bases 1 to 804)
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The HFB gene undergoes alternate splicing processes Blood Cells Mol. Dis. 26 (2), 155-162 (2000) 20448010
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The HFE gene undergoes alternate splicing processes
Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
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Pred. No. 3.9e-76;
0; Mismatches 1;
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                                                          Thenie, A., Orhant, M. and Mosser, J. Direct Submission Submitted (17-DEC-1998) UPR 41 CNRS, Pr. Bernard, Rennes 35043, France Location/Qualifiers
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                                                                                                                                                  1. .735
/organism="Homo sapiens"
/mol_type="mRNR"
/db_xref="taxon:9606"
/chromosome="6"
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Best Local Similarity 99.6%;
Matches 272; Conservative
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/gene="HFE"
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WITLAVPREERQRYCQYSHPGLDQPLIVIWEPSPSGTLVIGVIRGIAVFVVILFIGI
LFILLKRRQSRSEGMHYVLAFRE"

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE 99180629
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="hemochromatosis protein splice variant
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Homo sapiens hemochromatosis splice variant della
complete cds.
                                         Thenie, A., Orhant, M., Gicquel, I. and Mosser, J. Thenie, A., Orhant, M., Gicquel, I. and Mosser, J. Direct Submission.
Submission (1-MAY-1199) Faculte de Medecine, UP du Pr Leon Bernard, Rennes Cedex 35043, France Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 271.4; DB 9;
Pred. No. 3.9e-76;
0; Mismatches 1;
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Rhodes, D.A. and Trowsdale, J.
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Best Local Similarity 99.6% Y
Matches 272; Conservative (
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                             Rhodes, D.A.

Direct Submission
Submitted (21-JUL-1998) Immunology, University of Cambridge, Tennis
Court Road, Cambridge CB2 1QP, UK
Location/Qualifiers
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AJ249337.1 GI:15485422
alternative splicing; hemochromatosis protein; HFE gene.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens mRNA for hemochromatosis protein (HPE gene) splice
variant 3.
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37. .1041
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SGIAVFVVILFIGTLFILLRKRQSRGAMGHYVLAERE"
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SEG (HFE) MRNA,
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/function="iron metabolism"
/note="alternative splicing form wit deletion of complete
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2 (bases 1 to 100,000).
Oliva,R..
Direct Submission
Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic
Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic
Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGGAATTTCAAGCCAG
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Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y.,
David,V. and Mosser,J.
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                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                    /map="6p22"
/cell_line="HepG2"
1. .1073
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161. .931
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SLIFBALGYVDDQLFVFYDHSRRVEPRFPWSRSISSGWMGALGLSGSLKGWDHWFYDF
WITMENHHNSKESHTLQVILGFGEMQEDNSTESYWKYSYDGQDHLEFCPPTLDWRAAEP
RAWFTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVWTWARAEP
WYTTARCRAALNYYPQMITMKHIKDKQPMDAKEFEPKDVLPNGOGYPQUPTLAVPPGE
BORYTCQVBHPGLLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFILIRKRQG
SRGAMGHYVLAERE"
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                                                                                                               2 (bases 1 to 1200)
Thenle, A., Orhant, M. and Mosser, J.
Direct Submission
Submitted (1.20-1998) UPR 41 CNRS, Faculte de Medecine,
Pr. Bernard, Rennes 35043, France
Location/Qualifiers
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A soluble beta 2 microglobulin (beta2m)/hfe monochain for
biotechnological and therapeutic applications
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Blood Cells Mol. Dis. 26 (2), 155-164 (2000)
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/db_xref="GI:11094315"
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/gene="HFE"
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/protein_id="CAD35231.1"
/db_xref="G1:21440047"
/translation="MSRSVALAVLALLSLSGLBAIQRTPKIQVYSRHPAENGKSNFLN
CYVSGFHPSDIEVDLIKNGERIEKVBHSDLSFSKDWSFYLLYYTEFTPFEKDEYACRV
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TKEWRENK TRARQNRAYLBROCPADLQDLEBERGWTLDQVDFLVKVTHHVTSSYTT
IRCRALNYYPONITWKMLKOKQPMDAKEFERDVLPNDGTYQGWITLAVPPGEEQRY
TCQVEHPGLDQPLIVIWGLESRGPFEQKLISBEDLNMTGHHHHH"
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchinhashi,Z. and Wolff,R.K.
Hereditary herochromatosis gene products
Patent: US 6140305-A 9 31-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 271.4; DB 6; Length 1317;
Pred. No. 4e-76;
0; Mismatches 1; Indels 0;
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/note="unnamed protein product"
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                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic"
                                                               Location/Qualifiers
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/protein_id="CAD3
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Best Local Similarity 99.69
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                                                                                                     Unclassified.

1 (bases 1 to 1440)

1 (bases 1 to 1440)

Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihash, Z. and Wolff, R.K.

Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
hemochromatosis gene mutation
Patent: US 6228594-A 9 08-MAY-2001;
Location/Qualifiers
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 10 08-MAY-2001;
Location/Qualifiers
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Pred. No. 4.1e-76;
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Pred. No. 4.1e-76;
0; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 272; Conservative
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Hereditary hemochromatosis gene products
Patent: US 6140305-A 10 31-OCT-2000;
Location/Qualifiers
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.larity 99.6%; Pred. No. 4.1e-76;
Conservative 0; Mismatches 1; Indels 0;
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Pred. No. 4.1e-76;
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GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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                                                                                                                                        310 cargagagredecegrerogageeeeegaacrecargagrrrecagragaarrreaageeag 369
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                                                                                             CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
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Rothenberg B.E., Sawada-Hirai,R. and Barton,J.C. Mutations associated with iron disorders
Patent: US 6355425-A 1 12-WAR-2002;
Location/Qualifiers
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1.2e-76;
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0; Mismatches
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Sequence 1 from patent US 6355425.
AR199238
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/organism="unknown"
1 552 c 596 g
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WTIMENHNHEKVPPLVKVTHHYTSSYTTLRCRALNYYPQNITWKWLKDKQPNDAKEFE
PKDALPNGDGTYQGWITLAVPGEERRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVI
SGIAVPVVILFIEIILERRQGSRQAVGHYVLAERE"
1442 c 458 g 532 t
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    db xref="GI:11094325"
    translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFWGASEQDLGL
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Thenie,A., Orhant,M., Gicquel,I. and Mosser,J.
Direct Submission
Submitsed O-APR-1999) Faculte de Medecine, UPR41 CNRS, 2 Avenue
du Pr. Leon Bernard, Rennes Cedex 35043, France
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1885)
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                                                       GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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The HFE gene undergoes alternate splicing processes
Blood Cells Mol. Dis. 26 (2), 155-162 (2000)
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Pred. No. 4.1e-76;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                241 TGGACTATTATGGAAAATCACAACCACAGGAAG 273
                                                                                                                                                                                                                                                                                                                                               1. .1885
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p22"
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/gene="HFE"
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HOMO Sapiens haemochromatosis protein (HLA-H) mRNA, complete cds.
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1 (bases 1 to 2727)

Feder, J.N., Gnirke, A., Thomas, W., Tsuchihashi, Z., Ruddy, D.A.,
Basava, A., Dormishian, F., Domingo, R., Ellis, M.C., Fullan, A.,
Hinton, L.M., Jones, N.L., Kimmel, B.E., Kronmal, G.S., Lauer, P.,
Lee, V.K., Loeb, D.B., Mapa, F., McClelland, E., Meyer, N.C.,
Mintier, G.A., Moeller, N., Moore, T., Morkang, E., Prass, C.E.,
Ountana, L., Stranes, S.M., Schatzman, R.C., Brunke, K.J.,
Drayna, D.T., Risch, N.J., Bacon, B.R. and Wolff, R.K.
A novel MHC class I-like gene is mutated in patients with
                                                                                                                                                                                                                                                                                                           09
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Submitted (10-JUN-1996) Mercator Genetics, 4040 Campbell Ave., Menlo Park, CA 94025, USA
                                                                                                                                                                                                                                                                                                         1 GGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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Rothenberg, B.E., Sawada-Hirai, R. and Barton, J.C. Mutations associated with iron disorders Patent: US 650942-A 1 21-JAN-2003; Location/Qualifiers
                                                                                                                                                                                                               DB 6;
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Pred. No. 4.2e-76;
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Nat. Genet. 13 (4), 399-408 (1996)
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/mol_type="mRNA"
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AUTHORS
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RAMPTKLEWERHKIRARONDAYLERDCPAQLQQLLEGGRGVLDQQVPELVKVTHHVTS
SVTTLRCRALNYYPQNITMKMLKDKQPMDAKEFEPKDVLENGGGTVQGWITLAVPPGE
EQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIGVISGIAVFVVILFIGILFIILRKRQG
SRGAMGHYVLAERE"
                                                                                                                                                                                                                                                   SLFBALGYVDDQLFVFYDHESRRVEPRTPWVSRTSSQMMLQLSQSLKGWDHMFTVDF
WTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLBFCFDTLDWRAAEP
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                                                                                                                                                                                                                                   /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 11 31-OCT-2000;
Location/Qualifiers
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product="hatemochromatosis protein"

protein id="AAG51823.1"

db_xref="G1:1469790"
                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%; Score 271.4; DB 9;
99.6%; Pred. No. 4.2e-76;
live 0; Mismatches 1;
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db_xref="taxon:9606"
                                                                                             note="synonym: HFE"
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                  chromosome="6"
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                                                                                                               222. .1268
/gene="HLA-H"
                                    /map="6p21.3"
L. .2727
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Matches 272; Conservative
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 Search completed: February 11, 2004, 19:15:40 Job time : 1636.78 secs	ch compl time : 1	Sear Job
 528 TGGACTATTATGGAAAATCACAACACAAGAAAG 560	52	qq
 241 TGGACTATTATGGAAAATCACAACACAGGAAG 273	24	δδ
468 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCACTTCACTTGATGTTTTCACTTCACTTTCACTTCA	4.	qq
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 408 GAIGAGAGICGCCGIGIGGAGCCCCGAACTCCAIGGGIIICCCAGIAGAAIIICAAGCCAG 467	40	qq
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348 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 407	34	đ
 61 GGICTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120		Š
288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT 347	26	ΩD

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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM751283 54 bp mRNA linear EST 04-MAR-2002
K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kim YS
Genome Research Center
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Eceun-dong Yusecong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.
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                                                                                                                            BF465475
BBB165405
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CB960984
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BM751283.1 GI:19080901
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                                                                BM751283 K-EST0027
AU279987 AU279987
CB162561 K-EST0223
BF883952 PM4-ET020
                                                                                                  February 11, 2004, 15:39:52 ; Search time 1556.87 Seconds (without alignments) 4261.827 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB : Maximum DB :

Database

Result No.

Searched:

BU340705 AGENCOURT AU138140 AU138140 CB960984 AGENCOURT AL550540 AL550540 CA454707 AGENCOURT BQ924251 AGENCOURT

CD244248 AGENCOURT

AU132916 AU132916

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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
15418-52-3986
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
Hal human cDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa,A.; Fukuma,M.; Kusakari,S.; Hata,J.; Ishii,S.; Yamamoto,J.; Isono,Y.; Saito,K.; Nakamura,Y.; Masubo,Y.; Nagai,K.; Isogai,T.
HRI human cDNA project; cDNA library construction & 5'-end one Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                Contact: Takao Isogai
Genomics Laboratory
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/lab_nost="Toplof"
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1 (bases 1 to 560)

1 (bases 1 to 560)

1 (mabayashi, H., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Mori, T., Hata, J., Tomoya, Y. and Umezawa, A.

Redifferentiation of dedifferentiated chondrogues and chondrogenesis of human barrow stromal cells via chondrosphere formation with an expression profiling by large-scale cDNA analysis
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                                                    organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
71: +82-42-860-44770
                                                                                                                                                                                                                                                                 DB 9; Length 560;
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                      1;
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0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 TGGACTATTATGGAAATCACAACCACAGCAAG 374
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21C Frontier Korean EST Project 2001
                                                                                                                                                                                       124
                                                                                                                                                                                                                                                               Score 271.4;
                                                                                                  /cell_type="chondrocytes"
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/note="Vector: pME18SFL3"
/organism="Homo sapiens"
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 222.4; DB 1 Pred. No. 1.8e-59;
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99.2%;
                                    Tel: +55-11-2704922
Fax: +55-11-2707001
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1 (bases 1 to 384)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                /lab host="Top10F'"
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/clone lib="L17NG70205n1"
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Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
culture."
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                                                                                                                               /mol_type="mRNA"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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   Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: D column: 07
High quality sequence stop: 535.
Location/Qualifiers
                                                                                                              organism="Homo sapiens"
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/clone_lib="ET0209"
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
Vallet, J. Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush
J. and Keele, J.W.
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Email: asimpsonolludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seven in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&tL2=PM4-ET0209-151200-003-£07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stop: 384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 TITCCAGIAGAAITICAAGCCAGAIGIGGCIGCAGCIGAGTCAGAGICTGAAAGGGIGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCACATGITCACTGITGACTICTGGACTATTATGGAAAATCACAACCACAGCAAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF080089 523 bp mRNA linear
230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
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67_339.rst

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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mu89b05.rl Soares mouse lymph node NbMLN Mus musculus CDNA clone
IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I
HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 464)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 CTGTGGCTGCAGCTAAGCCAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               /tissue_type-_r./lab.host="DH10B"
/lab.host="DH10B"
/clohe=lab.etcor: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pltuitary, and placenta."
180 c 164 g 98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGGGCGGGGCACACTCCTGCTCTTCATGGGCGCCTCGGAGGCAGATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0%; Score 180.2; DB 12; Length 550; Best Local Similarity 78.8%; Pred. No. 5.2e-46; Matches 215; Conservative 0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGACTATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGACCATCATGGACAACCACAACTACAGCAAG 414
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Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                             scrofa"
                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 100 row: C column: 24
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                         Location/Qualifiers
1. .550
/organism="Sus scrof
                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA217236
AA217236.1 GI:1826237
  402 762 4366
402 762 4390
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DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                               /organish="mcNa"
/wol_type="mcNa"
/db_xref="taxon:9823"
/tissue_type="mcNa"
/tissue_type="pooled"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib=wARCZ_2PIG"
/note="Vector: pCNV SPORT6; Site_l: NotI; Site_2: SalI;
Library made from pooled tissue From testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
103 a 175 c 152 g 93 t
                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 550)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 GGGCTGCCCCTGTTTGAGGCCTTGGGCTACGTGGACGACCAGCTGTTTGTGTCTCTACAAT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ATGTGGCTGCAGCTGAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 CTGTGGCTGCAAGCTAAGCCAGAGAGCCTGAAAGGGTGGGATCACATGTTCACCGTGGACTTC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%; Score 180.2; DB 10; Length 523; 78.8%; Pred. No. 5e-46; ive 0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 bp mRNA linear
364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI339179
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGACCATCATGGACAACCACAACTACAGCAAG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mamm. Genome 13 (8), 475-478 (2002)
                                                                                                                                     PCR PRimers
FORWARD: AGGRAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 48 row: E column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                          organism="Sus scrofa"
                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 215; Conservative
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                       1. .523
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VERSION
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PUBMED
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BI339179
LOCUS
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Tel: 81-45-503-9222
Fax: 81-45-503-9225
Fax: 81-45-503-9226
Exai: 81-65-503-9226
Exai: 81-65-503-9216
Exai: genome.renegasc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramateu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii, Y., Yolto,M., Kavaii,Y., Kojian,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Takahashi,F., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TCCTTGTTTGAAGCTTTGGGCTACGTGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
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/cell type="B16 F10Y cells"
/clone lib="RIKEN full-length enriched, B16 F10Y cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="G370002P09"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse lymph node NbMLN"
hote="Yorgan: Lymph node; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
let strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                          Email: mouseest@watson.wustl.edu
This Clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:398537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 CTGCATCTGAGTCCAGAGCCTGAGAGGTGGGGCTACATGTTCATAGTAGACTTCTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 CCTTTGTTTGAGGCTAAGGGCTATGTGGATGACCAGCTCTTTGTGTCTACAATCATGAG
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 464;
                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 ATTAIGGAAAAICACAACCACAGGAAG 273
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                                                                                                                                                                                                                                                                                                                                                                    'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:652689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
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Matches 21
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/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="VI-M-CGOp-bik-d-03-0-UI"
/lab host="M1M BP Ret 4 S2"
/clone lib="W1H BMAP Ret 4 S2"
/note="Vector: pT7T3D-pac" (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Ecc RI; The
NIH BMAP Ret 4 S2 library is a subtracted library,
ultimately derived from mouse retina tissue library avarious stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enail: mESTGemail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP CDNA
Glones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP CDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine The following repetitive
elements were found in this CDNA sequence: 1-31, >(CAG
                                                        BE994943 489 bp mRNA linear EST 29-APR-2002 UL-M-CGOp-bik-d-03-0-UI.81 NIH BMAP_Ret4 S2 Mus musculus cDNA clone UI-M-CGOp-bik-d-03-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 489)
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Normalization and subtraction: two approaches to facilitate gene
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
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Fax: 301 443 9890
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Mus musculus

Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(EB (bazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,

Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,

Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A.,

Quackenbush, J., Schrimi, L.M., Kanapin, A., Matsuda, H., Batalov, S.,

Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaseterland, T., Gariboldi, M., Gissi, C., Godzik, A.,

Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,

King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons

Y. A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki,

H., Nagashima, T., Numaca, K., Ookido, T., Pavan, W.J., Percea, G.,

Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring

A. Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zammer, A.,

M., Sakzumen, N., Sato, K., Shiraki, T., Wahlestedt, C., Wang, Y.,

M., Sakzumen, N., Sato, K., Shiraki, T., Wahisa, Y., Yang, Y.,

Arakawa, T., Fukuda, S., Haro, A., Habizume, W., Imotani, K., Ishia

Y., Itoh, M., Kagawa, T., Yuan, Z., Zavolan, M., Waterston, R., Lander

B. S., Rogers, J., Birney, E. and Hayashizaki, Y., Waterston, R., Lander

B. S., Rogers, J., Shiraki, Y., Washizaki, Y., Waterston, R., Lander

B. S., Rogers, J., Shiraki, Y., Sakai, Z., Sasaki, D., Shibate

R. S., Rogers, J., Shiraki, P., Shiraki, A., Sakai, K., Sasaki, D., Shiraki, A., Shiraki,
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Acadehi,U., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
                                                                                                                                                      186
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TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
                                                                     119 CCTTTGTTTGAGGCTAGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG 178
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BY747346 RIKEN full-length enriched, 2 days neonate thymus thymic cells (NOD) Mus musculus CDNA clone B430034J19 5', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                      127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG
                                                                                                                                                                                                                                179 AGT CGC CGT GCT CAGGC CCC CGT CGAT CTT GGAGCAAACCT CAAGC CAGCT GT GG
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Mus musculus
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Fax: 81-45-503-9216
67
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                                                      SOURCE
                                                                                                                                                    Human Genome Sequences Mame. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust (MRC building Addenbrookes Hospital Cambridge) whose
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                                                                                                                                Computational Analysis of Full-Length Mouse cDNAs Compared with
'H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Sato,R., Sakazume,N., Sano,H.,
Sasaki,D., Saro,K., Shibata,K., Shizaki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/clone="E430034J19"
/tissue_type="thymus"
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/clone_lib="YXIXEN full-length enriched, 2 days neonate
thymus_thymic_cells (NOD)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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/strain="NOD"
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                                                                                                        Submission
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AK088986
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HTC 05-DEC-2002

AKOBB986 1719 bp mRNA linear HTC 05-I was musculus 2 days neonate thymus thymic cells cDNA, RIKEN Full-length enriched library, clone:E430034J19 product:hemochromatosis, full insert sequence.

AK088986

ACCESSION

DEFINITION

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Isahi, Y., Kayosawa, H., Kondo, S., Yamanaka, I., Saito, T., Golobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrinli, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Bolinga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K., Wang, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Bund Hayashizaki, Y. Gandida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Bund Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation 6 f60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1719)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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11217851
                                                                                                                                                   Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Nishi, K., Yosawa, H., Kondo, S., Yamanaka, I., Saito, T., Saito, T., Yamanaka, I., Saito, T., Ostazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Casaterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Fasole, G., Yochiwa, H., Wagner, L., Washlo, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Fletcher, C., Fullia, G., Blake, J., Boffelli, D., Bolinga, N., Fletcher, C., Fullia, M., Gariboldi, M. Gartinoin, S., Hill, D., Hofman, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L., Wynshaw-Borish, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Scholad, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Seboto, Cool, Seya, T., Shibata, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Sasaki, M. Wature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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358 CTGCATCTGAGTCAGAGCCTGAAAGGGTGGGACTACATGTTCATAGTAGACTTCTGGACC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                    AK009581

Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                 247 ATTATGGAAATCACAACCACAGCAAG 273
                                                                                                                                                             418 Arcardegecaacraraaccacagraag 444
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AK009581.1 GI:12844462
HTC: CAP trapper.
Mus musculus (house mouse)
Mus musculus
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AK009581
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KEYWORDS
SOURCE
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TLVKVTRHWASTGTSLRCQALDFFPQNITWRWLKDNQPLDAKDVNPEKVLPNGDETYQ
GWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLPLFEARCYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWIHLSQSLKGWDYMFI
VDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWRYGYDGQDHLEFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MSLSAGLPVRPLLLLLLWSVAPQALPPRSHSLRYLFMGASEPD"
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                                                                                                                            Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-3 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome_res@gec.riken.go.jp, URL:http://genome.gec.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 CTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 CCTTTGTTTGAGGCTAGGGGCTATGTGGATGACCAGCTCTTTGTGTGTCCTACAATCATGAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 TGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 AGTCGCCGTGCTGAGCCCCAGGGCCCCGTGGATCTTGGAGCAAACCTCAAGCCAGCTGTGG 357
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      Takaku-Akahira, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; hemochromatosis
(MGD|MGI:109191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 175.8; DB 11; Length 1719;
Pred. No. 2.2e-44;
0; Mismatches 57; Indels 0;
      Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-A)
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="FANTOM_DB:E430034J19"
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/db_xref="GI:26354116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="E430034J19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="NOD"
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BG747345.1 GI:14057998
                                      64.48;
78.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 819)
                                      Query Match
Best Local Similarity 78.7
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
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BG747345
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KEYWORDS
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DLGLPLFEARGYVDDQLFVSYNHESRRAEPRAFWILEQTSSQLWLHLSQSLKGWDYMF
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CPKTLIMGAAEPGAWATWYDDFHYTARQNRFDFEDFDGQV
PTLVKYTRHWASTGFSLRCQALDFFFQNITMRMLKDNOPELDAKDVNPERKYLPNGDETY
QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@geo.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Tel:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_st_gge="adult"
                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                    Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Marsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yasunishi, A., Yoshida, K., Tejima, Y., Toya, T., Yasunishi, A., Yoshida, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="unnamed protein product; hemochromatosis MGD|MGI:109191)
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/db_xref="MGI:1905246"
/db_xref="taxon:10090"
/clone="2310032M04"
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db_xref="GI:12844463"
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1. .1723
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                                                                               Nature 420, 563-573 (2002)
6 (bases 1 to 1723)
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1723
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                                                                                    JOURNAL
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/mol type="mknA"
// (Ind type="mknA")
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// (Ind type="adenocarcinoma cell line"
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                                                                                                                                                                                                                                                                                                                                   183 CCGCGTTCACATTCTCTAAGATACCTCTTCATGGGTGCCTCAGAGCCAGACCTCGGGCTG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 AGTCGCCGTGCCTGAGCCCAGGGCCCCGTGGATCTTGGAGCCAAACCTCAAGCCAGCTGTGG 362
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Tissue Procurement: ArCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 792.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                67 TCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                   Gaps
                                                                                                             0;
DB 11; Length 1723;
                                                                                                             Indels
                                                                                                  57;
Score 175.8; DB 1
Pred. No. 2.3e-44;
0; Mismatches 57
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/organism="Homo sapiens"
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Num Musculus Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 668)

S. Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, T., Nogami, A., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Datachil, M., Bradt, D., Eursic, V., Chothia, C. Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Farzer, K.S., Casaterland, T., Garibodi, M., Gissi, C., Godzik, A., Gugh, J., Grimmond, S., Gugtincich, S., Hirckawa, N., Jackson, I.J., Jarvis, B.D., Kanala, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, B.D., Kanagaya, A., Kurochkin, T.V., Lee, Y., Leharak, B. L., Konagaya, A., Kurochkin, T.V., Lee, Y., Leharak, B. L., Konagaya, M., Sandelin, M., Pertoskay, N., Jackson, I.J., McKenzie, L., Madjott, D.R., Revenaka, Y., Tavan, G., Setou, R. B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Sandelin, A., Schneider, C., Semple, C.A., Satou, K., Shimada, K., Sultana, R., Takenaka, Y., Tayan, C., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Wan, S., Yanan, S., Yanan, S., Yanaya, Y., Wang, Y., Sakawa, Y.,
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BY745026
                                                                                                                                                                                                                                                                                                                                                                                                            119 CCTTTGTTTGAGGCTAGGGCTATGTGGATGACCAGCTCTTTGTGTCCTACAATCATGAG
                                                                                                                                                                                                                                             7 CIGCGIICACACICICIGCACIACCICIICAIGGGIGCCICAGAGCAGGACCIIGGICII
                                                                                                             Score 174.8; DB 10; Length 392;
Pred. No. 2.3e-44;
0; Mismatches 58; Indels 0;
                             93
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TAG_SEQ=None found"
1 107 c 115 g
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                                                                                                                      64.0%;
78.3%;
                                                                                                                      Query Match
Best Local Similarity 78.3
Matches 209; Conservative
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/clone="VI-M-CGOp-bgp-a-01-0-UI"
/lab host="Wild (Life Technologies)"
/clone lib="Wild BMAP Ret4 52"
/clone lib="Wild BMAP Ret4 52"
/note="Vector: pT7T3D-Pac" (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco Ri; The
NIH BMAP Ret4 52 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP CDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP CDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The following repetitive elements were found in this cDNA sequence:
1.31, > (CAG)n#Simple_repeat
POLYA-NO.
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BMAP_Ret4_S2 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                  157 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 216
                                                                                                                                                                                                                                                                                                                   61 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I boasa; I to agas; Lossa; Lossa, M.B.
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                   1 caccadererreserrerrargareareardadarecederergadecededaderecarde 60
                                                                                                                                                                                                                                                                                                                                                                                                            217 GATCACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACACACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GACCAGCTGTTCGTGTTCTATGATCATGAGTGTCGCCGTGTGAGAGCCCCGAACTCCATGG
                                                                                               Gaps
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
2092-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                            .,
                                    DB 10; Length 819;
                             Query Match 64.2%; Score 175.4; DB 10; Length Best Local Similarity 99.4%; Pred. No. 2.1e-44; Matches 176; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 bp
UI-M-CG0p-bqp-a-01-0-UI.SI NIH Bl
UI-M-CG0p-bqp-a-01-0-UI 3', mRNA
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BF465475.1 GI:11534658
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EST 17-DEC-2002

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiror-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Email: genome-res@gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
VR.:http://genome-gec.riken.go.jp,
IRI:http://genome-gec.riken.go.jp,
VR.:http://genome-gec.riken.go.jp,
NR:http://genome-gec.riken.go.jp,
VR.:http://genome.gec.riken.go.jp,
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NR:http://genome-gec.riken.go.jp,
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NR:http://genome-gec.riken.go.jp,
NR:http://genome-gec.riken.go.jp,
VR.:http://w.itch,M., Rayashida,K., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohnato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,N., Watahiki,A., Muramateu,M. and Hayashizaki,Y. Direct
Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CIGCGITCACACTCICIGCACIACCICITCAIGGGIGCCICAGAGGAGCAGGACCIIGGICTI
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78.3%; Pred. No. 2.9e-44;
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/tissue_type="bone marrow"
/cell_type="macrophage"
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Contact: Yoshihide Hayashizaki
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273
1 cgcttgctgcgttcacactc......aaaatcacaaaccacagcaag 273
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result		Query				•
No.	Score	_	Match Length DB ID	DB	ΙD	Description
1	271.4	:	!	24	ABK49917	DNA encoding beta
7	271.4	99.4	1440	18		Hereditary haemoch
m	271.4			22	AAC68429	Human hereditary h
4	271.4		1440	22	AAC68430	Human hereditary h
Ŋ	271.4	99.4	2506	21	AAA96769	cDNA sequence enco
9	271.4		2727	19	AAV23525	Haemochromatosis q
7	269.8	98.8	1440	22	AAC68431	Human hereditary h
89	269.8	98.8	1440	22	AAC68432	Human hereditary h
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Human colon specif Hereditary haemoch Human hereditary h Human hereditary h Genomic DNA of a h Hereditary haemoch Hereditary haemoch Human hereditary h	human hin-H exon 2 Oligonuclectide D1 Oligonuclectide D1 Oligonuclectide D1 Oligonuclectide D1 Oligonuclectide D1 Human polynuclectide D1 Human secreted pro Human HFE peptide Bovine mammary tis DNA fragment with Probe used for gen CDNA encoding chic MHC class I antige MHC class I antige MHC class I antige Human MHC class I Chicken MHC class I Chicken MHC class I Chicken MHC class I Chicken MHC class I Worleic acid seque Human polynuclecti Human polynuclecti Human polynuclecti Human polynuclecti Human polynuclecti Human class Human secreted pro Sequence surroundi Human cDNA differe	### ALIGNMENTS #### ALIGNMENTS #### ABK49917; #### ABK49917; #### ABK49917; #### ALIGNMENTS #### ABK49917; ##### ABK49917; ##### ABK49917; ###################################
ABV93934 AAT96690 AAC68425 AAC68426 AAAC57926 AAV57926 AAV57928 AAC68428 AAC68428 AAT63897	AAH02414 AAF58231 AAF58232 AAF58236 AAF58246 AAF58246 AAF58246 AAC1392 AAA1266 AAA1266 AAA3266	ALIGNMENTS 317 BP. lobulin (beta2M)/HFE m n; beta2M/HFE monochai intracellular iron ab intracellular iron ab rin; receptor; TfR; br tissue damage; vascul sis; autoimmune diseas ne; ss. "beta2M/HFE monochain" "beta2M/HFE monochain"
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2 5 5 9 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	0 / / / / / / / / / / / / / / / / / / /	RESULT 1 ABK49917 ID ABK49917 XX BUT 15-JUL-2002 (XX BUMAn; beta 2 KW Human; beta 2 KW Aromorption absorption absorption after a control infect KW Aromorption infect KW Aromorption inflammation; KW inflammatory control inflammatory c
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RESULT 2

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The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

analogue or active fragment). linked to alphal-alpha3 domains of human

CHEE (a central regulator of iron absorption; undefined), or its analogue

or active fragment, by a flexible linker peptide, or a functional

Gerivative or all of (I). (I) is useful for reducing intracellular iron

absorption in patients having hereditary hemochromatosis, transflusions,

thalassaemias, haemolytic anaemia or chronic infections, and for

delivering a therapeutic to ceals that over-express transferrin receptor

(TfR) which are preferably lymphocytes or leukocytes, across the blood-

brain barrier. (I) is further useful for treating brain tumour. (I)

is also useful for treating oxidative stress disorders resulting in

ctissue damage e.g. vascular diseases, inflammation, atherosclerosis,

lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful

ctissue damage e.g. vascular diseases, inflammation, atherosclerosis,

lung injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful

ctissue damage e.g. vascular diseases, inflammation, atherosclerosis,

ctissue damage e.g. vascular diseases, inflammation, the monochain manifests

specific characteristics advantageous for drug delivery systems. It is a

soluble, stable and fully conformed protein. It binds specifically to

transferrin receptor. It is continuously internalised by the target cells, thus

calls, minimising aide effects. It negatively regulates iron absorption,

cells, minimising aide effects. It negatively regulates iron absorption,

cells, minimising efficient drug delivery.

cells, minimising efficient drug delivery in the staget cells that over-express

tris not diluted in the blood as is transferrin. It should not induce an

immune response since it is a self non-polymeric protein and delivery of

changes wing monochain is expected to overcome drug-resistance since it is a

coding sequence of beta2m/HFE monochain 
                                                                                                                                                                                                                                                                      Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                       UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                         Laham N;
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 2; 77pp; English.
                                                                                                                                      Rotem-Yehudar R,
  22-SEP-2000; 2000US-234843P.
                                                                                                                                                                                       WPI; 2002-383192/41.
P-PSDB; AAU80035.
                                                                              MCINNIS P.
                                                                                                                                                                                                                                                                                                                                                              a linker peptide
                                                                                                                                   Ehrlich R,
                                                                              (MCIN/)
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Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other; coding sequence of beta2m/HFE monochain.

WPI; 1997-512743/47. P-PSDB; AAW36499

> ö 462 120 522 180 582 240 642 09 ATGREGATICAGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAAAGGTTCACATGTTCACATGTTCACTTCA 463 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 403 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT CATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTTCCAGTAGAATTTCAAGCCAG CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT Gaps Score 271.4; DB 24; Length 1317; Pred. No. 2.7e-79; 0; Mismatches 1; Indels 0; IGGACTATTATGGAAAATCACAACCACAGCAAG 273 TGGACTATTATGGAAAATCACAACCACAGCAAG 675 99.4%; Conservative Local Similarity 272; 523 181 583 643 Н 61 121 241 Query Match Matches qq ₹ g g à g ò g à

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/*tag= i
/note= "G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                               /*tag= g
/note= "C to G substitution (24d2 mutation)
                                                                                                                                              results in His to Asp substitution"
                                                                                                                                                                          results in Ser to Cys substitution'
                                                                                                                                                                    "A to T substitution (24d7 variant)
                                                             Hereditary haemochromatosis; metal toxicity; diagnosis;
                                                                                                                                                                                                                                                                                                                  Thomas WJ;
                                                Hereditary haemochromatosis gene cDNA clone.
                                                                     gene therapy; prenatal screening; human; ss
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                                                                                                 Location/Qualifiers
222.1268
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      AAT96691 standard; cDNA; 1440 BP
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96US-0630912.
96US-0632673.
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                                 (first entry)
                                                                                                                                                                                                                                                                                                                   Drayna DT, Feder JN, Gn.
Isuchihashi Z, Wolff RK;
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16-AFR-1996;
                                                                                    Homo sapiens
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                                                                                                                                                      variation
                   AAT96691;
                                                                                                                        mutation
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AAT9669
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Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a Cys to Tyr substitution in the encoded protein (see AAW36499) at a Cys to Tyr substitution in the encoded protein (see AAW36499) at a Critical disulphide bridge important for secondary structure. The following are claimed: a 10825 bp genomic DNA sequence (1) (see AAT96690), the 1437 bp cDNA sequence (Ta) and their 24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method mutation; an animal model for the HH disease; metal chelation Disclosure; Fig 4; 115pp; English.

Thu Feb

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agents, T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of ino overload, a method for screening potential therapeutic agents for activity in connection with HH disease; an antisense oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotides covering a range of nucleotides from (1), (1a) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening cor for HH homozygotes, to HH disease, including gene therapy, protein- and antibody-based therapeutics, and small molecule
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Pred. No. 2.8e-79;
0; Mismatches 1; Indels
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272; Conservative
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                                                                                                                                                            alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                      288 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                            The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                       Score 271.4; DB 22; Length 1440;
Pred. No. 2.8e-79;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuchihashi Z,
                                                                                                                                                                                                             Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human hereditary hemochromatosis 24d1 mutation cDNA
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                                                                 Disclosure; Fig 4; 108pp; English
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96US-0652265.
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Matches 272; Conservative
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16-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                           The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
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for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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S65C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene, chromosome 6p; iron disorder; haemochromatosis; ss.
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"if this base is mutated to G, then protein contains the mutation H63D"
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                                                                                                                                                                                                                                                        Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
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                                                                                                                                                                                                                                                                                            Score 271.4; DB 2:
Pred. No. 2.8e-79;
0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) mon-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the aisorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number U60319). The presence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
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"if this base is mutated to C, then the protein contains the mutation I105T, which is associated with an iron overload disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barton JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sawada-Hirai R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BILL-) BILLUPS-ROTHENBERG INC
                                                                                                                                                                                                                                                                                                                                                                                 99US-0277457.
                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000WO-US07982.
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                                                                                                                                                           WO200058515-A1
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This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample encompassing all or part of the DNA between markers D6S265 and D6S276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an autosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD.

CE precially the method is used to diagnose HH or predisposition to HH by detecting a Cys282Tyr substitution. Individuals homozygous for this mutation have HH and heterozygotes are potential carriers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGIGGCIGCAGCIGAGICAGAGICIGAAAGGGIGGGAICACAIGIICACIGIIGACIIC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 cargadacrececereredadececedaacrecardecrirecagradarricaageeag 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GETCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GECTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
                                                                                      Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 271.4; DB 19; Length 2727; Pred. No. 3.6e-79; 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                  (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                           Cullen LM, Jazwinska EC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page -; 32pp; English
                                                                                                             autosomal recessive disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 99.4%;
Local Similarity 99.6%;
New 272; Conservative
                                                                                                                                                                                                                                                                               97WO-AU00539
                                                                                                                                                                                                                                                                                                                        96AU-0002083
                                                                                                                                                                                                                                                                                                                                         96AU-0001849
               (first entry)
                                                        Haemochromatosis gene.
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                                                                                                                                                                                                                                                                                   22-AUG-1997;
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                 10-JUL-1998
                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                          26-FEB-1998.
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Best Local S
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Powell LW;

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121 CATGAGTGTCGCCGTGTGGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 GATGAGAGTCGCCGTGTGGACCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 CGCTTGCTGCGTTCACACTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGTCTTTCCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 GGICTTICCTTGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal
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                                                                                                                                                                                          Human hereditary hemochromatosis 24d2 mutation cDNA
                                                                                                                                                                                                                        H; hereditary hemochromatosis; chelation agent;
-cell differentiation factor; iron overload; ss.
273
               Gnirke A, Ruddy D,
241 TGGACTATTATGGAAAATCACAACCACAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chelation agent alleviating iron overload
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96US-0632673.
96US-0652265.
                                                                                                     AAC68431 standard; DNA; 1440
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                                                                                                                                                               (first entry)
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ses 271; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-006341/01.
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23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feder JN;
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241 TGGACTATTATGGAAAATCACAACCACAGCAAG 273

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The present invention relates to human colon specific nucleic acids (ABV9310-ABV94009) and proteins (ABP68360-ABP6435). The nucleic acids and proteins are useful for treating colon cancer and colon disorders, and diagnosing or monitoring the presence of colon disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated colon-specific nucleic acid molecule, useful for treating colon cancer, and diagnosing or monitoring the presence of metastases
                                                                                                                                                                                              Human, colon, cytostatic, vaccine, gene therapy, colon cancer, colon disorder, metastasis, ds.
 528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
                                                                                                                                                                   Human colon specific nucleic acid, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastases of colon cancer in a patient
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                                                                             ABV93934 standard; DNA; 5982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of colon cancer in a patient
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolff RK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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                                                                                                                                                                                Human hereditary hemochromatosis 24d1/2 mutation cDNA.
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                                                                                                                                                                                                            HH; hereditary hemochromatosis; chelation agent;
T-cell differentiation factor; iron overload; ss
TGGACTATTATGGAAATCACAACCACAGCAAG 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drayna DT, Gnirke A,
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                                                                                          AAC68432 standard; DNA; 1440
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Conservative
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96US-0652265.
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nes 271; Conserv
                                                                                                                                                                                                                                                         Homo sapiens
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23-MAY-1996;
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                                                                                                                       AAC68432;
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3521 3461 o, 130 190 70 3462 IGITIGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3402 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 71 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3522 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 191 AGCTGAGTCAGAGTCTGAAAGGCTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT Gaps Length 5982; ; Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other; 1; Indels Query Match 95.8%; Score 261.4; DB 25; Best Local Similarity 99.6%; Pred. No. 1e-75; Matches 262; Conservative 0; Mismatches 1; 1

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3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881
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extending from D6S265, which is a marker that is centromeric of extending from D6S265, which is a marker that is centromeric of than, in a telemeric direction through D6S265, a marker at which the allelic association was no longer observed. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 66% of affected chromosomes and in 4% of unaffected chromosomes. It results in a Cys to Tyr substitution in the encoded protein (see AM36499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH genomic DNA (1), a 1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and 24d7, variants; a cloning or expression vector; host cells; a 24d7 variants; a cloning or expression vector; host cells; a 24d7 variants; a cloning or expression of a least 56 amino acid residues of these; an antibody produced using the peptide; a method cesidues of these; an antibody produced using the peptide; a method cesidues of the pressness or absence of the common HH gene mutation; an animal model for the HH disease; metal chelation agents, T-cell differentiation factors and therapeutic agents for mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in conceining or creating a method for screening product of a nucleic acid sequence as above; and oligonucleotide directed against a transcriptional creating and therapeutic agents for relatively in connection with HH disease; an antisense oligonucleotide directed against a transcriptional creating and produced in the HH gene. The invariants, useful for detecting a polymorphism in the hypoxygores, to HH disease, including gene therapy, the hypoxygores, to HH disease, including gene therapy, the hypoxygores is and therapeutics, and small molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
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Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This genomic DNA sequence corresponds to the human gene whose mutated form is associated with herediteary haemochromatosis (HH). To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region
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/note= "G to A substitution (24d1 mutation
associated with HH), results in Cys
Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 115pp; English.
                                                                                                                 Hereditary haemochromatosis gene.
              AAT96690 standard; DNA; 10825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERC-) MERCATOR GENETICS INC
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/note= "C :
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Tsuchihashi Z, Wolff RK;
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P-PSDB; AAW36499.
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04-APR-1996;
16-APR-1996;
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Wolff RK;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3762 GTTCACACTCTCTGCACTACCTCTTCATGGCTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                   Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cch 95.8%; Score 261.4; DB 22; al Similarity 99.6%; Pred. No. 1.3e-75; 262; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                     Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                           chelation agent alleviating iron overload -
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                                                                                                                                                                                                                                     Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 3; 108pp; English.
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                                                                                                               96US-0630912.
96US-0632673.
96US-0652265.
                                                                            97US-0834497.
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                                                                                                                                                                                                                                     Thomas WJ, Drayna DT,
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                                                                            04-APR-1997;
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23-MAY-1996;
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US6140305-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                     Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                    New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%; Score 261.4; DB 22; Length 10825; 99.6%; Pred. No. 1.3e-75; cive 0; Mismatches 1; Indels 0; 0
                                                                                                                                                                                                                                     Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
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96US-0632673.
96US-0652265.
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tes 262; Conserv
                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB36869.
                                                                            04-APR-1997;
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23-MAY-1996;
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Best Loca Matches

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Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.

Homo sapiens

Genomic DNA of a histocompatibility iron loading (HFE) gene.

Human hereditary hemochromatosis 24d1 mutation DNA HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.

Homo sapiens

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e.g. haemochromatosis, or a genetic susceptibility to develop it.
                      Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;
                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barton JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 21-28; 55pp; English.
               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BILL-) BILLUPS-ROTHENBERG INC
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10206..10637
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/number= 5
7995..9050
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652..4915
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                                                                                                                                            TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC
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                                                                                                                                                                                                                GCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCCAAGCCAGATGTGGCTGC
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                                   Indels
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DB 21;
Score 261.4; DB 21;
Pred. No. 1.4e-75;
0; Mismatches 1;
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AAV57926 standard; DNA; 235033 BP.
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Query Match 95.8%;
Best Local Similarity 99.6%;
Matches 262; Conservative
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i Z, Wolff RK;
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haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual, and (b) assessing the
DNA or RNA for the presence or absence of a haplotype or genotype where
the presence or absence of the haplotype genotype indicates the likely
presence of the HFE gene mutation in the genome of the individual. The
products for use in the diagnosis and treatment of HFE. The present
invention also describes BTF genes, which are homologues of the milk
protein butyrophilin (BT), and can be used in the production of agonists
and arreagonists of BT function. Also described are: (1) a RoRet gene
which can be used to develop products for the study, diagnosis and
treatment of lupus and Sjogren's syndim transport gene, and can
which are homologues of a type I sodium transport gene, and can
similarly be used for hypophosphatemia.
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43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149 13268 GCCGTGTGGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGGCTGC 43209 43329 43269 ó 130 131 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 250 43388 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC 11 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 0; Gaps Query Match
95.8%; Score 261.4; DB 19; Length 235033;
Best Local Similarity 99.6%; Pred. No. 4.8e-75;
Matches 262; Conservative 0; Mismatches 1; Indels 0; G Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other; 43148 IGGAAAAICACAACCACAGCAAG 43126 251 TGGAAATCACAACCACAGCAAG 7.1 191 엄 ਨੋ à 임 d 셤 ð Š

Hereditary haemochromatosis subregion from an HH affected individual AAV57903 standard; DNA; 237326 BP (first entry) Homo sapiens 21-DEC-1998 AAV57903; AAV57903/c RESULT 15

Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.

39-APR-1998

97WO-US17658 30-SEP-1997;

97US-0852495 96US-0724394 07-MAY-1997; 01-OCT-1996;

(PROG-) PROGENTIOR INC.

Thomas WJ; Ruddy DA, Feder JN, Kronmal GS, Lauer PM, Tsuchihashi Z, Wolff RK;

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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HFB) affected individual. ABO described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the by providing DNA or RNA for the presence or absence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The products for use in the diagnosis and treatment of HFB. The present products for use in the diagnosis and treatment of HFB. The present products for use in the diagnosis and treatment of HFB. The present invention also describes BTF genes, which are homologues of the milk products for the study, diagnosis and antagonists of BT function. Also described are: (1) a ROREt gene which are homologues of a type I sodium transport gene, and can can milarly be used for hypophosphatemia.
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                                         Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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                                                                                                                                                                                present invention describes hereditary haemochromatosis gene
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                                                                                                                                    Claim 1; Fig 9; 209pp; English
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WPI; 1998-240014/21.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: OZ-MAY-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
US-10-158-057-105
US-10-272-655-110
US-10-273-321-110
US-10-273-321-110
US-10-273-256-110
US-10-273-256-111
US-10-273-228-110
US-10-273-228-1110
US-10-273-232-130687
US-10-027-632-130689
US-10-027-632-130689
US-10-027-632-130689
US-10-027-632-130689
US-10-027-632-130689
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US-10-027-632-130689
US-10-027-632-130689
US-10-28-28-21
US-10-28-38-812
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Prayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchhashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY: USA
ZIP: 10036-2711
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COMPUTER READABLE FORM:
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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100.0%; Score 273; DB 13; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1.8e-86;
Matches 273; Conservative 0; Mismatches 0; Indels 0;
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| Publication No. US20030148972A1
| GENERAL INFORMATION: Thomas, Winston J. Drayna, Dennis T. Feder, John N. Gnirke, Andreas Ruddy, David Tsuchihashi, Zenta Wolff, Roger K. TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 79
| CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                             8907-095-999
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US-10-138-888-77
                                 NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-900
TELEPHONE: (212) 869-8864
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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STATE: New York
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /phenotype= "normal or wild-type
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                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04.APR-1997
APPLICATION NUMBER: US 08/652,265
                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                 FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: replace(408,
OTHER INFORMATION: /phe
(unaffected)"
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: replace(414,
OTHER INFORMATION: /phe
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 222..1268
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DB 13; Length 1440;
Score 271.4; DB 13; Length
Pred. No. 6.9e-86;
0; Mismatches 1; Indels
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Best Local Similarity 99.6%;
Matches 272; Conservative
   99.4%;
ilarity 99.6%;
Conservative
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US-09-981-606-1
   Query Match
Best Local Similarity
Matches 272; Conserva
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   468 AIGIGGCIGCAGCIGAGTCAGAGTCIGAAAGGGGGGGAICACAIGIICACTGTIGACTIC 527
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LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                           US-10-138-888-10
| Sequence 10, Application US/10138888 |
| Sequence 10, Application US/10138888 |
| Publication No. US20030148972A1 |
| Publication No. US20030148972A1 |
| Publication No. US20030148972A1 |
| Partition No. US20030148972A1 |
| Feder, John N. |
| Gairke, Andreas |
| Ruddy, David |
| TITLE OF INVENTION: Hereditary Hemochromatosis Gene |
| NUMBER OF SEQUENCES: 79 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pennie & Edmonds LLP |
| STREET: 1155 Avenue of the Americas |
| CITY: New York |
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHAX: (212) 790-9090
TELEPHAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                            TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURREMY APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTONEY/AGENT INFORMATION:
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US-10-138-888-10
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222..1268
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                                                                                                                                                                 181 ATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC
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                                             1 CGCTTGCTGCGTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTT
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  Gaps
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Pred. No. 8.7e-86;
0; Mismatches 1; Indels 0;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09981606

Sequence 1, Application No. US20030129595A1

GENERAL INFORMATION:

APPLICANT: Rothenberg et al.

TILLE OF INVENTION: Mutations associated with iron disorders
FILE REFERENCE: 24065-004CON

CURRENT PILING DATE: 2002-10-16

CURRENT APPLICATION NUMBER: 09/277,457

PRIOR PILING DATE: 1999-03-26

NUMBER CF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LINGTH: 2506
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US-10-138-888-11
; Sequence 11, Application US/10138888
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121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
                                                                   408 GATGAGAGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 467
                                                                                                                              181 ATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGGATCACATGTTCACTGTTGACTTC 240
                                                                                                                                                                              468 Argregerecadereagreagagrereaaagegregeareacargrecaegregeres 527
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. POSISBANE
RAGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 28,07-095-999
                                                                                                                                                                                                                                  TGGACTATTATGGAAAATCACAACCACAGCAAG 273
                                                                                                                                                                                                                                                                                     528 redacrarraredaaaarcacaacacaaa 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allele
replace(408, "g")
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                      US-10-138-888-12; Sequence 12, Application US/10138888; Publication No. US20030148972A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Winston J. Drayna, Dennis T. Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
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                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.8%; Score 269.8; DB 13; Length 1440; Best Local Similarity 99.3%; Pred. No. 2.5e-85; Matches 271; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                    Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION - Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,265
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 24d2
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                             APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFHONE: (212) 790-90
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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222..1268
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STRANDEDNESS: single
Publication No. US20030148972A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CATGAGTGTCGCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ATGTGGCTGCAGCTGAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
(HH)"
                                                                                                                       NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                       Query Match
98.8%; Score 269.8; DB 13; Length 1440;
Best Local Similarity 99.3%; Pred. No. 2.5e-85;
Matches 271; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 TGGACTATTATGGAAAATCACAACCACAGCAAG 560
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APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 23-MAY-1996

FILING DATE: 23-MAY-1996

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                               /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZEP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
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                                                                          label= 24d2
                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-138-888-79
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Sequence 25, Application US/10016634A
Sequence 25, Application US/10016634A
Publication No. US20020192666A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Profunce application NUMBER: US/10/016,634A
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,258
PRIOR PILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 176
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                           REGISTRATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 8907-095-999
TELECOMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEFAX: (212) 790-9090
THER INFORMATION: /product= "Hereditary Hemochromatosis (HI) protein containing the 24d7 mutation"
/note= "Hereditary Hemochromatosis (HI)gene 24d7 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 263; DB 13;
100.0%; Pred. No. 1.6e-82;
tive 0; Mismatches 0;
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FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                  5507..6023
                                                                                                                                                                                                                                                                                                                                   140..7319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= 24d7
                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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3821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                       "Hereditary Hemochromatosis
                                                                                                                                                          (HH) protein"
/note= "No. US20030148972Almal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 95.8%; Score 261.4; DB 13; Length Best Local Similarity 99.6%; Pred. No. 6.1e-82; Matches 262; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drayna, Dennis T.
Feder, John N.
Ghirke, Andreas
Ruddy, David
THULE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9000
TELEPAX: (212) 869-8864
OTHER INFORMATION: /product= "Heredit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: 5507..6023
                                                                                                                                                                                                                                                                                                 LOCATION: 140..7319
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                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
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                                                                                                                                                                                                                           Score 261.4; DB 14; Length 5982; Pred. No. 4.7e-82; O; Mismatches 1; Indels O;
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Gnirke, Andreas
Ruddy, David
Tauchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-MAy-2002
CLASSIFCATION: CURKOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/834,497
FILING DAYE: 04-APR-1997
FILING DAYE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,265
APPLICATION NUMBER: US 08/632,673
FILING DAYE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DAYE: 04-APR-1996
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                            CTHER INFORMATION: n=a, c, g or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (5885).. (5885)
CTHER INFORMATION: n=a, c, g or t
US-10-016-634A-25
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6%;
Matches 262; Conservative (
                NAME/KEY: misc feature
LOCATION: (5780)..(5780)
OTHER INFORMATION: n=a, c, g
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LENGTH: 12146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing the 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.8%; Score 261.4; DB 13; Length 10825; Best Local Similarity 99.6%; Pred. No. 6.1e-82; Matches 262; Conservative 0; Mismatches 1; Indels 0;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION UMBER: 28 462
REGISTRATION NUMBER: 28 462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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OTHER INFORMATION: /pro
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gene 24d1 allele"
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LOCATION:
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; Sequence 27, Application US/09981606; Publication No. US20030129595A1; GENERAL INFORMATION:

US-09-981-606-27

RESULT 11

APPLICANT: Rothenberg et al.

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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.8%; Score 261.4; DB 13; Length 12146; Best Local Similarity 99.6%; Pred. No. 6.4e-82; Matches 262; Conservative 0; Mismatches 1; Indels 0;
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: 08/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
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OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
PILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4892 TGGAAATCACAACCACAGCAAG 4914
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10301844 Publication No. US20030100747A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruddy, David A. Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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43338 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 GCCGTGTGGAGCCCCCGAACTCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 190
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                                                                                                                                                                                                                          Length 237326;
                                                                                                                                                                                                                          Score 261.4; DB 15; Length
Pred. No. 2.4e-81;
0; Mismatches 1; Indels
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
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APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CJRRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43098 recahantelandaneen 43076
                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                    LENGTH: 237326 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drayna, Dennis T.
                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feder, John N.
                                                                                                                                                                                                                          95.8%;
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Best Local Similarity 99.6
Matches 262; Conservative
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APPLICANT: Thom
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US-10-138-888-5
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                                                                                                                                                                                                                                                                  Score 261.4; DB 15; Length 235033; Pred. No. 2.4e-81; O; Mismatches 1; Indels O; Gč
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESE for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION PATA:
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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FILING DATE: 07-MAY-1997
                                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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         TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 235033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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99.6%;
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ZIP: 10036-2811
                                                                                                                                                                                                                                                                                       Best Local Similarity
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Search completed: February 11, 2004, 22:07:07 Job time : 236.656 secs
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PRIOR APPLICATION DATA:
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LOCATION:
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                                                                              (HH) protein containing the 24d2
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Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 9
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                       95.2%; Score 259.8; DB 1 99.2%; Pred. No. 2.3e-81;
             REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEPAX: (212) 869-8864
OTHER INFORMATION: /product= "Heredit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                       ; LOCATION: 5507..6023
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-138-888-5
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APPLICANT: Thomas, Winston J.
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 NAME: Brian M. Poissant
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NAME/KEY:
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US-10-138-888-7
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                                                           FILING DATE: 23-MAY-1996

FILING DATE: 16-APR-1996

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Polssant

REGISTRATION NUMBER: 28,462

TELEPANINICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEPAX: (212) 865-8864

CTHER INFORMATION: /product= "Hereditary (HH) protein containing both the 24d1

and 24d2 mutations"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
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SEQUENCE DESCRIPTION: SEQ ID NO:
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February 11, 2004, 15:39:51 ; Search time 904.219 Seconds (without alignments) 6831.698 Million cell updates/sec
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1 aacatcaccatgaagtggct.....gcagagatatacgtnccagg 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                  2888711 seqs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR097991 Sequence AR117804 Sequence AR117804 Sequence AR117805 Sequence AR149474 Sequence AR149476 Sequence 182157 Sequence 182157 Sequence 182157 Sequence 182157 Sequence 182157 Sequence 182157 Sequence 182158 Sequence 182157 Sequence AR184234 Homo sapi AF079409 Homo sapi AF079409 Homo sapi AF079409 Homo sapi AF079407 Homo sapi AF17795 Sequence AR117795 Sequence AR117795 Sequence AR117796 Sequence AR117796 Sequence AR117791 Sequence	A linear PAT 14-FEB-2001 acid and method of making
ID	AR097991 AF525359 AR117804 AR117804 AR117805 AR149475 182157 182157 182157 182157 182157 182167 AF7079409 AF184234 AF079409 AF079409 AF184234 AF079409 AF115265 AF0794033 AF0794033 AR117794 AR117794 AR117794 AR117799 AR117790 AR117791	360 bp DNA 2248 27, C.P.H. 23-JUN-2000;
% Query :e Match Length DB	150 150 150 150 150 150 150 150	AR097991 360 bp DNJ Sequence 5 from patent US 6074825. AR097991. GI:12807248 . Unknown. Unknown. Unclassified. 1 (bases 1 to 360) 1 (bases 1 to 360) Rundell,C.A. and Vary,C.P.H. Stable encapsulated reference nucleic Patent: US 6074825-A 5 13-JUN-2000;
Result No. Scor	0 10	RESULT 1 AR097991 LOCUS DEFINITION S ACCESSION P VERSION KEYWORDS SOURCE ORGANISM TEFFERENCE 1 AUTHORS FILLE JOURNAL E

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Unknown.
Unclassified.
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ACCESSION
VERSION
KEYWORDS
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ORIGIN
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 479)
Kutlar,F., Glendenning,M. and Kutlar,A.
Heterozygote C-->G mutation in intron 3 of human hemachromatosis gene detected on a caucasian individual with beta thalassemia trait Unpublished
                                                                                                                                                                                                                                                                                                                                                         AF525359 479 bp DNA linear PRI 24-JUL-2002
Homo sapiens hereditary hemochromatosis protein HLA-H precursor
(HFB) gene, exon 4 and partial cds.
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Kutlar, F., Glendenning, M. and Kutlar, A.

Kutlar, F., Glendenning, M. and Kutlar, A.

Submitted (27-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
Laboratcory, Medical College of Georgia, 15th Street, AC-1000,
Augusta, GA 30912, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAM82608.1"
/db_xref="G1:21952518"
/translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
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precursor"
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                                                                       Score 150; DB 6;
Pred. No. 2e-36;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="6"
              /organism="unknown"
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/sex="male"
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I (bases 1 to 517)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW"
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Pred. No. 2e-36;
0; Mismatches 1; Indels
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Pred. No. 2e-36;
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Sequence 20 from patent US 6140305.
AR117804
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Patent: US 6140305-A 20 31-OCT-2000;
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Sequence 21 from patent US 6140305.
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/gene="HFE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 517)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 20 08-MAY-2001;
Location/Qualifiers
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140335-A 21 31-0CT-2000;
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Seguence 21 from patent US 6228594.
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Sequence 20 from patent US 6228594.
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PAT 10-JUN-1998
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            Unclassified.

1 (bases 1 to 517)

Thomas,W.J. Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatcosis gene mutation
Patent: US 6228594-A 21 08-MAY-2001;
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Tsuchihashi, Z., Gnirke, A., Thomas, W.J., Drayna, D.T., Ruddy, D., Wolff, R.K. and Feder, J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic
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Pred. No. 2e-36;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                            Length 517;
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Location/Qualifiers
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Sequence 3 from patent US 5712098.
182157
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120 c 146 g
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Tsuchinashi,Z., Gnirke,A., Thomas,W.J., Drayna,D.T., Ruddy,D.,
Wolff,R.K. and Feder,J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic
                                                                                                                    1 (bases 1 to 517)
Tsuchinashi, Z., Gnirke, A., Thomas, W.J., Drayna, D.T., Ruddy, D., Wolff, R.K. and Feder, J.N.
Hereditary hemochromatosis diagnostic markers and diagnostic
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Patent: US 5712098-A 13 27-JAN-1998;
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Sequence 13 from patent US 5712098.
182167
182167.1 GI:3210464
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Location/Qualifiers
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182158 517 bp
Sequence 4 from patent US 5712098.
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/organism="unknown"
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/codon_start=3
/product="hereditary hemochromatosis protein precursor"
/protein id="hARL16502.1"
/db_xref="GI:13241988"
/translation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFERDKUPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW"
                                                                                                                                                                                                                                                                       Kutlar,F., Holley,L., Glendenning,M. and Kutlar,A.
A new compound heterozygotes IVS4-48G/A/IVS4-115T/C polymorphism of
HFE gene found in an Africa American individual with mild anemia
Unpublished
                                PRI 07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 551)
Kutlar,F., Holley,L., Glendenning,M. and Kutlar,A.
Direct Submission
Submitted (21-DEC-2000) Medicine/Hemoglobin DNA Laboratory, Sickle
Cell Center, Medical College of Georgia, 15th street, AC-1000
                                                                                                                                                                                                      Bukaryoïa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
551 bp DNA linear PRI 07-MAR-Homo Sapiens hereditary hemochromatosis protein precursor (HFE) AF331065
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|gene="HFE"
|note="HLA-H precursor; putative iron-binding ligand
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replace="g"
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/note="heterozygous polymorphism"
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/cell_type="WBC"
/tissue_type="whole_blood"
/looe="HFB"
/looe="HFB"
/gene="HFB"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="6"
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/gene="HFE"
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/gene="HFE"
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/gene="HFE"
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2 (bases 1 to 733)
Kutlar, F., Glendenning, M. and Kutlar, A.
Kutlar, F., Glendenning, M. and Kutlar, A.

Submitsed (28-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA
Laboratory, Medical College of Georgia, 15th street, AC-1000,
Augusta, GA 30912, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF525499 133 bp DNA linear PRI 04-AUG-2002
Homo sapiens hereditary hemochromatosis protein precursor (HFE)
194 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 253
                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                              L (Dasse 1 to 733)
Kutlar,F., Glendenning,M. and Kutlar,A.
Heterozygote T->C mutation was detected at the intron 4 of thuman hemachromatosis gene in an Africa American individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .733
/organism="Homo sapiens"
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/isolation_source="African-American individual"
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/map="6p21.3"
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6
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|oin(<114. .389,548. .>661)
|gene="HFE"
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gene="HFE"
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                                                   254 CCTGGGGAAGAGCAGAGATATACGTGCCAGG
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'note="heterozygote"
'replace="t"
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replace="a"
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/cell_type="WBC"
<1. .>733
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'gene="HFE"
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AF525499
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TITLE
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Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica -
IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
(FG), ITALY
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                                                                                                  200 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 259
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                                                                                                                                              61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                               1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAAGGAGTTCGAACCT
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          Score 150; DB 9; Length 551; Pred. No. 2e-36; 0; Mismatches 1; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="6p22"
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'usedin=Y09801:hfe_mrna
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/usedin=Y09801:hfe_mrna
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5.
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H.sapiens HFE gene, exon 4 &
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Location/Qualifiers
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              Query Match
Best Local Similarity 99.3%;
Matches 150; Conservative
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51. .326
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/gene="HFE"
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Gasparini, P.
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Homosapiens Hemochromatosis splice variant delE2(14E4) (HFE) mRNA, AF079409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hemochromatosis splice variant delE214E4"
/protein id="AAC62649.1"
/brotein id="AAC62649.1"
/db xref="d1:3695111"
/translation="morrarphilmentalized"
/translation="morrarphilmentalized"
EGYWKYGYDGQDHLEFCPDTLDWRAREPRAPTKLEWERHXTRARQNTAYLERDCPAQ
TYQGHITLAYPPGERGYTLOXQYTTRAYPQUITHKWLKDKQPMDAKEFEPKDVLPNGDG
TYQGHITLAYPPGERGYTTQVPHPGLDQPLIVIWEPSPSGGTLVIGVISGIAVFVVII
FIGILFILEKRQGSRGAMGHYVLAERE"
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Catarrhini, Hominidae; Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
1 (bases 1 to 781)
Alternate 1 to 781)
Alternate splice variants of the hemochromatosis gene Hfe
Immunogenetics 49 (4), 357-359 (1999)
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                                                                                                                                              Length 772
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Pred. No. 2e-36;
0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
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 note="homozygous"
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/codon_start=1
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1. .781
                   /replace="a"
564. 677
/gene="HFE"
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37. .777
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tränslation="PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE
FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWEPSPSGTLVIG
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 772)
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'product="hereditary haemochromatosis protein precursor"
'protein id="AAF01222.1"
'db_xref="G1:6010711"
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens hereditary haemochromatosis protein precursor (HFE) gene, partial cds.
                                                                                       197 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                      1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                    linear
                 Indels
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/cell_type="white blood cell"
<1. .>772
                                                                                                                                                                                                                                                                                                                                      DNA
Pred. No. 2e-36;
; Mismatches
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join(<130. .405,564. .>677)
/gene="HFE"
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AF184234
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380 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 439
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                                      121 CCTGGGGAAGAGCAGAGATATACGINCCAGG 151
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Submitted (04-NOV-1999) Oliva R., Human Genome Research Group,
Faculty of Medicine and Clinic Hospital, Casanova 143, 08036, SPAIN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            HSA250635 809 bp mRNA linear PRI 03-NOV-2001
Homo sapiens mRNA for Hemochromatosis protein (HFE gene), DELEXZ+3
splice form.
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QVEHPGLDQPLIVIWEPSFSGTLVIGVISGIAVFVVILFIGILFIILRKRQGSRGAMG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                61 AAAGACGTATIGCCCAAIGGGGAIGGGACCIACCAGGGCIGGAIAACCTIGGCIGIACCC
                                      1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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Sequence:

Searched:

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Minimum Maximum

Database

Result

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CK82180 100012 MA
BK479663 IG6329 BA
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCWA40 row: j column: 04
High quality sequence stop: 566.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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AZ025590
AX088986
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AX030695
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BM723847 UI-E-E01-
CB529554 UI-H-FT2-
BG747345 602704818
                                                                         February 11, 2004, 15:39:52; Search time 861.127 Seconds (without alignments) 4261.827 Million cell updates/sec
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              5.1.6
Compugen Ltd.
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               GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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BM723847
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Matches 150; Conservative
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                                                                                                              /clone="INGES:3544803"
/tissue_type="renal cell adenocarcinoma"
/lab.host="NHIOB (phage-resistant)"
/clone lib="NHI MGC 14"
/note="Organ: kIdney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synchesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Fax: 310 335 9565

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I (bases I to 668)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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UI-E-EO1-aix-h-17-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
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99.3%; Score 150; DB 10; Length 570;
Best Local Similarity 99.3%; Pred. No. 5.8e-33;
Matches 150; Conservative 0; Mismatches 1; Indels
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                               organism="Homo sapiens"
                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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/done libe Wille Technologies) (it jurge lebistum)
/done libe Wille Wetor: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-E01 is a normalized cDAA library containing the
following tissue(8): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDAA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDAA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDAA contains a library tag
sequence that is located between the Not I site and the
(dT):8 tail. The sequence tag for this library is
CGGGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI):
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UI-H-FT2-bjh-m-12-0-UI.sl NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjh-m-12-0-UI 3', mRNA sequence.
                                 /dev_stage="fetal"
|Jab_host="DH10B (Life Technologies) (T1 phage resistant)"
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Email: cgapba-remail.nih.gov

Trissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

POLYA=Yes.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Pred. No. 6.2e-33;
0; Mismatches 1;
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type="fetal eye"
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/db_xref="taxon:9606"
/clone="lmAGE:4857941"
/tissue_type="adenocarcinoma cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
                                                                     tissue type="Aveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 150; DB 14;
Pred. No. 6.4e-33;
'db_xref="taxon:9606"
'clone="UI-H.FT2-bjh-m-12-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 CCTGGGGAAGAGCAGATATACGTGCCAGG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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211 c 165 g
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BG747345.1 GI:14057998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.3
Matches 150; Conservative
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Best Local 8
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LOCUS
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Unitarior. susy, suson bepartment of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Baail: szhao@filpir.org
Email: szhao@filpir.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (infr@resgon.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 316 row: A column: 10
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ025590 1444 bp DNA linear GSS 25-FEB-2000 RPCI-23-316A10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316A10
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 444)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG (G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Strategne) and Superscript II RT (Life Technologies)" a 201 c 235 g 181 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         537 AACATCACCATGAAGTGGCTGAAGGATAAGCAG-CAATGGATGCCAAGGAGTTCGAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                           Length 819;
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                                                                                                                                                                                                                                                                                                                                                           Score 126; DB 10;
Pred. No. 5.7e-26;
                                                                                                                                                                                                                                                                                                                                 83.4%; Sco. No. 5.0. 98.0%; Pred. No. 5.0. 0; Mismatches
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/strain="C57BL/6J"
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/clone="RPCI-23-316A10"
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/clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 148; Conservative
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ECORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACG3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watchiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Nas musculus 2 days neonate thymus thymic calls cDNA, RIKEN
full-length enriched library, clone:E430034019
product:hemochromatosis, full insert sequence.
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                                                                                                                                                                                                                                                        Length 444;
                                                                                                                                                                             1 others
                                                                                                                                                                                                                                                     Match 55.9%; Score 84.4; DB 28; Local Similarity 72.2%; Pred. No. 4.6e-14; les 109; Conservative 0; Mismatches 42;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincin,S., Hill,D.,
Hofmann,M., Hume,D.A., Kaniya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,T., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1719)
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics evellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) Whose assistance we gratefully acknowledge.
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/db_xref="taxon:10090"
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/protein_id="BAC40688.1"
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/db_xref="G1:26354116"
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                                                                                                      PKTLNWSAAEPGAWATKVEWDEHKIRAKONRDYLEKDCPEQLKRLLELGRGYLGQOVP
TLVKVTRHWASTGTSLRCQALDFFPQNITWRWLKDNQPLDAKDVNPEKVLPNGDETYQ
GWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVGI
LFLILRKRKASGGTMGGYVLTDCE"
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/mol_type="mixm" and color of the property of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPKTLAWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKNCPEQLKRLLELGRGYLGQQV
PTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVLPNGDETY
QGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
                                                              'tissue_type="tongue"
'clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B1452668 831 bp mRNA linear EST 21-AUG-2001 603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       834 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCC 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.llhl.gov.prow: j column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nlh.gov
Tisaue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Paparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                      Anote="unnamed protein product; hemochromatosis
(MGD|MGI:109191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 1723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.4; Db .r.,
~~d. No. 7.8e-14;
~~a 42; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 7.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccreeceaccaccaccaccreccreccac 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILFLILRKRKASGGTMGGYVLTDCE"
                                                                                                                                                                                                                                                                                                               protein id="BAB26373.1"
|db_xref="GI:12844463"
|db_xref="MGI:109191"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 818.
Location/Qualifiers
clone="2310032M04"
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                                                                                                                     'dev_stage="adult"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative"
                                                                                                                                                                                                                                                                                     codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI452668.1 GI:15243324
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Best Local Similarity 72.2%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 C
                                                                                                                                                                                                                                                        putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyA_site
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
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AUTHORS
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KEYWORDS
SOURCE
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BI452668
LOCUS
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                                                                                                                                                         CDS
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Other_GSSS: RPCI-23-408J22.TV
Contact: Shaying Zhao
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pierer de Jong
(pietradejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://popac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPCI-23-408J22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22 AZ074871
                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                            62 TAACGGGGATGAGACCTATCAAGGCTGACATTGGCCGTGGCCCCTGGGGACGAGAC 121
                                                                                                                                                                                                                                                                                                                                      75 CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGAGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 536)
                                                                                                                                                                                                                                                                        2 dregricaadeacaaccaaccacregareccaaagarercaacceeagaagereracce
                                                                                                                                                                                                           15 GTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCC
                                                                                                                                                    Gaps
                                                                                       Length 831;
                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse BAC End Sequences from Library RPCI-23
                                                                                   48.7%; Score 73.6; DB 12;
70.8%; Pred. No. 7.7e-11;
iive 0; Mismatches 40;
215 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
189 g
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AAGGTTCACCTGTCAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 GAGATATACGINCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ074871.1 GI:7367768
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/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3 6; Site 1:
Fore 1: Site 2: EcoR1; Female C57BL/67 mouse kidney and/or
Broni Site 3: EcoR1; Female C57BL/67 mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 135 c 112 g 108 t
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/mol_type="mRNN"
/mol_type="mRNN"
/db_xref="taxon:9796"
/clone lib="Mesenteric lymph node (MLN1)"
/note="Organ: Mesenteric lymph node; Vector: pBluescript
SK(-) from Lambda ZaplI; Site_1: EcoRI; Site_2: EcoRI; The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM781326 473 bp mRNA linear EST 05-MAR-2002 MLN1 7_F05.g1_A005 Mesenteric lymph node (MLN1) Equus caballus cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Perissodactyla; Equidae; Equus.
1 (bases I to 473)
Watson, J.L., Vandenplas, M., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Moore, J. and Pratt, L.H.
An EST database from equine (Equus caballus) mesenteric lymph nodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 GAGAAGGIGCIACCIAACGGGAAIGAGACCIAICAAGAGGGGGGTAA--AAGAAAGIGGCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AACATCACTATGAGGTGGATGAAGGACAACCACCAGGATGCCAAAGATGTCAACCCC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Faz: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65.6; DB 28; Length 481; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 CCTGGGGACGAGACAAGGTTCACCTGTCAAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
/db_xref="taxon:10090"
/clone="RPCI-23-316C10"
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High quality sequence stop: 473
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                                                                             /sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM781326.1 GI:19129558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Equus caballus (horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.4%;
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ORIGIN
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BM781326/c
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                                                                                                                                                           /lab host="unioud"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCORI; Site_2: BCORI; Female C57BL/6J mouse kidney and/or
Bcori; Site_2: BCORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
BCORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
... 134 g 114 t lothers
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RPCI-23-316C10.TV RPCI-23 Mus musculus genomic clone RPCI-23-316C10
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,S., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. Mouse, BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 AACATCACTATGAGGTGGTTGAAGGACAACCAACCACTGGATGCCAAAGATGTCAACCC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 GAGAAGGIGCTACCTAACGGGGAIGAGACCTATCAAGGCTGGAT-GCATTAACCGTGGCC 140
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Email: szhaogtigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

plate: 316 row: C column: 10
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Other GSSs: RPCI-23-316C10.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70.8; DB 28
Pred. No. 4.2e-10,
0; Mismatches 43
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/mol type="qenomic DNA"
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/strain="C57BL/6J"
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Matches 107; Conservative
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library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass
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MAK030695 2032
Mus musculus 10 days neonate head cDNA, RIKEN Full-length enriched library, clone:5530400118 product:hypothetical Major hitocompatibility complex protein, Class I containing protein,
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                                                                                                                                                                                                                                                                                                   361 CACTCTGACCTGGCTTCTGGATGGGGAGCCCATGCACCAGGGCACCTTTGGGCCTAGGGC 302
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                                                                                                                                                                                                                                                 6 CACCATGAAGTGGCCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGA
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Magner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Teletcher, C., Fulita, M., Gariboldi, M., Gustinoich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Hill, D., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaertes, P., Nordone, P., Sato, R., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whitcaker, C., Wilming, L., Mahnaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, M., Hirameto, K., Hirameto, F., Hivasane, T., Harameto, K., Hirameto, F., Hivasane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sanch, K., Saitch, H., Sakai, C., Sakai, K., Sakazume, N., Sanch, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagama, M., Tagawa, A., Takada, X., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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'db xref="GI:26326681"
'translation="MLLSRNLRALAAIHLMIVYLLLEDLLGTCAEGDNQRLVASAPYQ
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DSQEPRIKDHLRAETWGRETDDLQEEEEQLKGMLAEITAQNGQNTDLHILQATFGCEL
QRNGSTRGFWKLGYDGQNFLIFPDQKTLTWTVDGPSTQKNKTLMKTRAPRADLVKAFLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
& 60,770 &111-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2338)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama 20-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9222, Fax:81-45-503-9222, Fax:81-45-503-9222, Gonome Exploration Research Group in Rik Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL.http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db xref="taxon:10090"
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/strain="C57BL/6J"
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Righ, B., Tomita, M., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Maner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Bassh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Huwe, D.A., Kamiya, M., Lee, N.H., Lyons, F., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 2490)

S Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,M., Hiramcto,K., Hiraoka,T., Harotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamira,M., Nishi,K., Nomura,K., Niyazaki,A., Murata,M., Nishi,K., Satio,R., Sakai,C., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Takaku,T., Tanaka,T., Tomaru,A., Toyau,T., Takahashi,F., Takaku-Akahira,S., Takaka,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Exploration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Tel:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
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histocompatibility complex protein, Class I containing
protein (InterPro IPR001039, evidence: InterPro)
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Please visit our web site for further details.
URL:http://fantome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/clone="4732481C10"
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/strain="C57BL/6J"
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AUTHORS
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        DI CPAQLQRYLASLRNGLLNTGFPKVI VTFRNY PVGRITLTCRAFRLYTRVATLTWLQ
YRKPVQQKTFGSETILLPSGDGTYQAWVSIRVLPGQESQFSCNLKHGNHNINEPAATEA
PVYGARREQPPTSGVGSRVGKSLWSAMTTALVVI SWTLSQKLMGPLLWFCSGGFCSFL
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AK029010.1 GI:26324971
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Best Local Similarity 62.7%;
Matches 79; Conservative (
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/db_xref="G1:26324972"
/translation="MLLSRNLRALAAIHLWIVYLLLEDLLGTCAEGDNQRLVASAPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical Center, HHMI; 5323 Harry Hines Blvd, Dallas, TX 75235-9050, USA (E-mail:YOSHINO@UTSW.SWMED.EDU, Tel:214-648-5047, Fax:214-648-5453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1074 CACCCTGACCTGGCTTCAGTATAGAAAGCCAGTACAGCAGAAAACCTTTGGATCTGAAAC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1134 TATCCTGCCCAGTGGGGATGGCACCTACCAGGCCTGGGTGTCCATTCGGGTTCTTCCTGG 1193
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 0.00055;
0; Mismatches 53;
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/strain="BALB/c"
/db_xref="taxon:10090"
/chomosome="17"
/clone="cosmid 12.1"
/haplotype="H2d"
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/organism="Mus musculus"
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2 ACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTA 61

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Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
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281 rádágaccagóccrocadgógárddaáccrrccadaagrdógcadcrefideredrecerd 340
                                                                                  62 AAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCC 121
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1 (bases 1 to 710)
Smith, T.P. L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
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/clone_lib="MarG GBOV"
/clone_lib="MarG GBOV"
/note="Vector: pcDNH3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pitultary, and
placenta/endometrium.
205 c 249 g 102 t
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732494 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
CB466784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4369 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1%; Score 48.4; DB 14; Best Local Similarity 65.4%; Pred. No. 0.0014; Matches 70; Conservative 0; Mismatches 37;
                                                                                                                                                                                                  122 CTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                            341 TTGGGAAAGAGCAGAGTTACACATGCCATG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LAMB009 row: C column: 12
Seg primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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/organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
Contact: Smith TPL
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Haemochromatosis g Human musculoskele cDNA encoding nove

Human hereditary

Hereditary haemoch Human hereditary h Human hereditary h Human hereditary h Human hereditary h Genomic DNA of a h Hereditary haemoch Oligonucleotide DI Oligonucleotide DI Human HLA-H exon 4 Human HLA-H exon 4 Human polynucleoti Human polynucleoti

Human polynucleoti Human polynucleoti Human polynucleoti Human breast cell Human foetal liver Probe #14690 for g Human bone marrow Probe #14109 for g Probe #14109 for g Probe #3729 used t Human liver single

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Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane; membrane; senembrane stability; test cell; molecular diagnosis; genetic testing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biological preparation of a stably encapsulated reference nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary hemochromatosis gene target nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
          AAA96769
AAV23525
AAL36747
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ABK83570
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AAI63974
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AAI24176
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                                                                                                                                                                                                                   AA16397
  AAX16055 standard; DNA; 359
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2225
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19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                       2004, 15:39:51 ; Search time 111.113 Seconds (without alignments) 3668.467 Million cell updates/sec
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                                                                                                                                        .....gcagagatatacgtnccagg
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                          2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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AAC68440
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AAC68430
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                                                                                                                                     1 aacatcaccatgaagtggct...
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Maximum DB seq length: 2000000000
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Score 150; DB 22; Length 517; Pred. No. 1.2e-39; 0; Mismatches 1; Indels (

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120 242

302

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243 AAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                                                              183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                              61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                                                                                                                                                                                                              1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                     products. These proteins may be used to treat a patient diagnosed a having human hemochromatosis disease. It is also useful as a metal callation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replace therapy for individuals having a defective human hemochromatosis ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human hereditary hemochromatosis DNA used for mutation detection.
                                                                                                                                          Sequence 517 BP; 126 A; 120 C; 147 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HH; hereditary hemochromatosis; chelation agent;
T-cell differentiation factor; iron overload; ss
                                                                                                                                                                                                                                                                                                                                                                               121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                             303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG
                                                                                                                                                                            99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                          Query Match
Best Local Similarity 99.3
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-006341/01.
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23-MAY-1996;
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ID AAC6
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                                                          The present sequence represents a nucleic acid sequence that is used as a reference sequence to exemplify the method of the invention. The specification describes a method for the biological preparation of a stably encapsulated reference nucleic acid for molecular diagnostic and genetic testing. The method comprises inserting a vector containing a reference nucleic acid into a cell through its lipoprotein outer membrane to encapsulate the nucleic acid, multiplying the cell to propagate the nucleic acid, multiplying the cell to propagate the and achieving a desired stability of the cell membrane for substantially matching the nucleic acid with the membrane stability of test cells. The reference nucleic acid with the membrane stability of test cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                        Length 359;
 for molecular diagnostic and genetic testing
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                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                     Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                        ; DB 20;
1.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruddy D,
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 1
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                                 5; Page 48; 51pp; English
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96US-0632673.
96US-0652265.
                                                                                                                                                                                                                                                                                                                     99.3%;
99.3%;
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.3
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC68440 standard;
 nseful
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23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                      Query Match
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                               Claim
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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                      Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                  Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                  Gnirke A, Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 6, 108pp; English
                                                                  96US-0630912.
96US-0632673.
96US-0652265.
97US-0834497
                                                                                                                                                                                                                   (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                              Drayna DT,
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New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal

chelation agent alleviating iron overload

Disclosure; Fig 6; 108pp; English

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Key
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                                                                                                                    120
                                                                                         242
                                                                                                                                 243 AAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGGGCTGGATAACCTTGGCTGTACC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a soluble polypeptide (I) of beta 2 microglobulin (beta2m)/HFE monochain comprising human beta2m (or its analogue or active fragment), linked to alphal-alpha3 domains of human HFE (a central regulator of iron absorption; undefined), or its analogue or active fragment, by a flexible linker peptide, or a functional derivative or salt of (I). (I) is useful for reducing intracellular iron absorption in patients having hereditary haemochromatosis, transfusions,
                                                                9
                                                                                                                                                                                                                                                                                                                                                                                  iron absorption regulator; intracellular iron absorption; lung injury; haemochromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR; brain tumour; cancer; oxidative stress disorder; itssue damage; vascular disease; inflammation; atheroscierosis; autoimmune disease; inflammatory condition; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                        183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                    AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC
                                                               1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                         Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
                                      0;
               Length 517;
                                                                                                                                                                                                                                                                                                                                              DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                                      Indels
                                        1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "beta2M/HFE monochain"
            Score 150; DB 22;
Pred. No. 1.2e-39;
0; Mismatches 1;
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                                                                                                                                                                        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                             303 CCTGGGGAAGAGCAGAGATATACGTACCAGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laham N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 2; 77pp; English.
                                                                                                                                                                                                                                                                  ABK49917 standard; cDNA; 1317
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               99.3%;
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                                                                                                                                                                                                                                                                                             ABK49917;
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               Query Match
Best Local
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thalassaemias, haemolytic anaemia or chronic infections, and for delivering a therapeutic to cells that over-express transferrin receptor (TER) which are preferably lymphocytes or leukocytes, across the bloodbrain barrier. (I) is further useful for treating brain tumour. (I) is also useful for treating oxidative stress disorders resulting in tissue damage e.g. vascular diseases, inflammation, atherosclerosis, cum injury, isofaemia, etc. A DNA molecule (II) encoding (I) is useful as a platform for drug delivery of therapeutic use for cancer, autoimmune diseases and inflammatory conditions. The monochain manifests specific characteristics advantageous for drug delivery systems. It is a coupuble, stable and fully conformed protein. It binds specifically to transferrin receptor (TER) and therefore targets cells that over-express this receptor. It is continuously internalised by the target cells, thus cells, minimising side effects. It dissociates from the receptor in the cells, minimising side effects. It megatively regulates iron absorption. It is not diluted in the blood as is transferrin. It should not induce an immune response since it is a self non-polymeric protein and delivery of drugs via monochain is expected to overcome drug-resistance since it is a continuous of herear in the present sequence represents the continuous of herear monochain sequence represents the
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"G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1317;
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"C to G substitution (24d2 mutation)
results in His to Asp substitution"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 24;
Pred. No. 1.6e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding sequence of beta2m/HFE monochain.
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222.1268
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ilarity 99.3%;
Conservative (
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Best Loca
Matches
              RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                               This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally clonded plasmid-based cDNA library following identification of the HH locus in the HHA region of chromosome 6. A single mutation (24d1) in the HH gene a general responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The following are claimed: a 10825 bp genomic DNA sequence (1) (see AAP19669), the H437 bp cDNA sequence (1a) and their 24d1, 24d2 and 24d7, oar iants: a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants contact these forms and 24d7, or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method codetermine the presence or absence of the common HH gene and taining and liferentiation factors and therapeutic agents for the HH disease; metal chelation agents. T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the respectic of a nucleic acid sequence as above; and oligonucleotide directed against a transcriptional therapeutic agents for activity in connection with HH disease; an artisense oligonucleotide directed against a transcriptional the produce or pairs of oligonucleotide directed against a transcriptional the mitigation of involections also relates to methods for screening of the HH gene. The invanincian also relates to methods for screening diagnosis, and therapeutics, and small molecule for the hardened in the properties of the hardened in the properties of
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Pred. No. 1.6e-39;
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                                                                                                                                                                                  Thomas WJ;
                                                                                                                                                                                                                                                                        Hereditary haemochromatosis gene and variants - usefi
and treatment of hereditary haemochromatosis disease
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0; Mismatches
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                                                                                                                                                                                    Gnirke A,
                                                                                                                                                     (MERC-) MERCATOR GENETICS INC.
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96US-0632673.
                                                           97WO-US06254.
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Z, Wolff
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                                                                                                                                                                                                 Fsuchihashi Z,
 WO9738137-A1
                                                           04-APR-1997;
                                                                                        23-MAY-1996;
                                                                                                        04-APR-1996;
16-APR-1996;
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                              16-0CT-1997
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981 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040
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                                                                                                                                                                                                                 HH; hereditary hemochromatosis; chelation agent; r-cell differentiation factor; iron overload; ss
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                                                                                                                                                               Human hereditary hemochromatosis cDNA.
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AAC68429 standard; DNA; 1440 BP
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96US-0632673.
96US-0652265.
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16-APR-1996;
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Wolff RK;

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products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                            New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to hereditary hemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150; DB 22; Length 1440;
Pred. No. 1.6e-39;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                               Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human hereditary hemochromatosis 24d1/2 mutation cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; 88.
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                                                                                                                                                                                               Ruddy D,
                                                                                                                                                                                               Drayna DT, Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 108pp; English
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Best Local Similarity 99.3%;
Matches 150; Conservative (
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96US-0632673.
96US-0652265.
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16-APR-1996;
23-MAY-1996;
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                                                                                                  16-APR-1996;
23-MAY-1996;
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                                       04-APR-1997;
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31-OCT-2000
                                                                                                                                                                                                 Thomas WJ,
                                                                                                                                                                                                                    Feder JN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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                                                                                                                                                                                                                                                                                                                                                                                Gnirke A, Ruddy D, Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hereditary hemochromatosis 24d2 mutation cDNA.
    Human hereditary hemochromatosis 24d1 mutation cDNA.
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                                           HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
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23-MAY-1996;
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/product= "histocompatibility iron loading (HFE) protein"
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                                                                                                                                                                              The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-call differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequence encoding a histocompatibility iron loading (HFE) protein.
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              Wolff RK;
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S65C"
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                                                                                                                                                                                                                                                                                                                  99.3%; Score 150; DB 22; Length 1440; 99.3%; Pred. No. 1.6e-39; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
                Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "if this base is mutated to G, protein contains the mutation
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                                                                                                                                                                                                                                                                                       Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 other;
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                Ruddy D,
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                Gnirke A,
                                                                                                                                                   Disclosure; Fig 4; 108pp; English.
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Matches 150; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene laad to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The method given in A96769 (Genbank Accession number U60319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
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/*tag= f // hote= "if this base is mutated to C, then the protein contains the mutation I105T, which is associated with an iron overload disorder"
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Pred. No. 1.9e-39;
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Best Local Similarity 99.3%;
Matches 150; Conservative
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14-AUG-2000;
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14-AUG-2000;
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                                                                           Homo sapiens.
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23-AUG-2000;
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                                                                                                                                    02-AUG-2001
This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D6S265 and D6S276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an cutosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cya282Tyr substitution. Individuals homozygous for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980
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                                                                                                                                                                                                                                            Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
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                                                                                                                                                                                  Cullen LM, Jazwinska EC, Powell LW;
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                                                                                                                                                      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                                                                                          Disclosure; Page -; 32pp; English.
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                                                                            97WO-AU00539
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96AU-0001849
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23-AUG-1996;
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vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0205515.
2000US-0209467.
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2000US-0239937.
2000US-0241221.
2000US-0241786.
2000US-0241786.
2000US-024186.
2000US-0241809.
2000US-024181809.
2000US-024181826.
2000US-024181826.
2000US-024617.
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29-SEP-2000;
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08-NOV-2000
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The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human proventing in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and prevention of: (a) cancer, e.g. breast and ovarian cancer and coher cancers of the atrenal gland, bone, bone marrow, breast, other cancers of the adrenal gland, bone, bone marrow, breast, and sleenes e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, and tiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discorders such as myocardial ischaemias; (d) wound condity, e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1748 AAGACGTATTGCCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1807
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                                                                                                                                                                                                              Isolated polypeptide for treating, preventing and or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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Pred. No. 2.5e-39;
0; Mismatches 1;
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                                                                                                                                    Ruben SM;
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                                                                                         (HUMA-) HUMAN GENOME SCI INC.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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Rosen CA, Ruben SM, WPI; 2003-128199/12.

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keratinocyte growth, hair loss, melanocyte growth, cell proliferation, cell growth, organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin, percentage of adipose tissue, pigmentation; cosmetic surgery; metabolism; blorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; endorine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content;
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2000US-229343P. 2000US-229344P. 2000US-229345P. 2000US-229509P. 2000US-229513P. 2000US-231413P. 2000US-234223P. 2000US-225270P. 2000US-225447P. 2000US-225757P. 2000US-234997P. 2000US-235834P. 2000US-236327P. 2000US-236367P. 2000US-220964P. 2000US-224518P. 2000US-228924P. 2000US-229287P. 2000US-218290P. 2000US-220963P. 2000US-236368P. 2000US-236369P. 2000US-217487P. 2000US-225267P 000US-225268P. 000US-225758P. 000US-226868P. 2000US-234274P 2000US-237037P 17-JAN-2001; 2001US-0764877 2000US-236370P 2000US-236802P 000US-237038P 2000US-237039P nutritional component. JS2002147140-A1 13-OCT-2000; 2 20-OCT-2000; 2 20-OCT-2000; 2 02-0CT-2000; 02-0CT-2000; 02-0CT-2000; 02-0CT-2000; Homo sapiens. 14-AUG-2000; 05-SEP-2000; 05-SEP-2000; 08-SEP-2000; 21-SEP-2000; 25-SEP-2000; 29-SEP-2000; 02-OCT-2000; 14-AUG-2000; 10-OCT-2002

08-DEC-2000; 2000US-251869P

ROSEN C A. RUBEN S M. BARASH S C.

(RUBE/) (BARA/) ROSE/)

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The invention describes an isolated nucleic acid molecule couprishing a gequence encoding misculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or the mucleic acid; stimulates re-vasculariastion of isohaemic tissues associated with conditions such as thrombosis, arterioscierosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis conditions, such as, Alzheimer's disease, Parkinson's disease, and neurohal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue cransports or bone grafts; prevents skin aging due to sunburn by stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains or stimulates growth used in combination with other cytokines; maintains correases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases or decreases the differentiation or proliferation of embryos; increases increases or decreases or decreases or decreases or decreases
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                                                                                           Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer -
                                                                                                                                                                                                                The invention describes an isolated nucleic acid molecule comprising a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
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                                                                                                                                                                 Disclosure; SEQ ID NO 3112; 321pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1998 (first entry)
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WPI; 1997-512743/47.
P-PSDB; AAW36499.
        Homo sapiens
                                                                                  WO9738137-A1
                                                                                           04-APR-1997;
                                                                                               23-MAY-1996;
                                                                                                 04-APR-1996;
16-APR-1996;
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                                                             variation
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5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748
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It results in a Cys to Tyr substitution in the encoded protein (see AAW34499) at a critical disulphide bridge important for secondary structure. The following are claimed: the HH gene motor DNA (1), a 1437 bp CDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and 24d7, variants; a cloning or expression vector; host cells; a cestidues of these; an antibody produced using the peptide; a method residues of these; an antibody produced using the peptide; a method contained of the common HH gene mutation; an animal model for the HH disease; metal chelation agents, T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of iron overload; a method for screening potential. Therapeutic agents for activity in connection with HH disease; an injeanse oligonucleotide directed against a transcriptional product of antiense oligonucleotide seawow; and oligonucleotides from cor pairs of oligonucleotides covering a range of nucleotides from cor pairs of oligonucleotides covering a range of mucleotides from the HH gene. The HH gene. The hH gene. The hH gene. The hH denney relates to methods for screening for the HH homovycores to the HH corrects.
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                                                                                                                                                                                                                                                                                                                                                                                                                     for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy, protein- and antibody-based therapeutics, and small molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150; DB 18;
Pred. No. 2.9e-39;
0; Mismatches 1;
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96US-0632673.
96US-0652265.
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Best Local Similarity 99.3%;
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary hemochromatosis (HH). To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region of chromosome 6. A physical clone coverage was then generated extending from D65255, which is a marker that is centromeric of HLA-A, in a telomeric direction through D65276, a marker at which the allelic association was no longer observed. A single mutation (24d) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes.
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"G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
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"C to G substitution (24d2 mutation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     results in His to Asp substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       results in Ser to Cys substitution
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"A to T substitution (24d7 variant)
                             Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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96US-0630912.
96US-0632673.
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Isuchihashi Z, Wolff RK;
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Gaps

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Wolff RK;

WPI; 2001-006341/01

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                               New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.3%; Pred. No. 2.9e-39;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
                                                                                                                                                                   Disclosure; Fig 3; 108pp; English.
                         P-PSDB; AAB36869
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5809 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 5839 CCTGGGGAAGAGAGATATACGTNCCAGG 151

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Search completed: February 11, 2004, 18:33:15 Job time : 112.113 secs

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1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCAATGCCAATGCCAAGGAGTTCGAACCT

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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Sequence 11, Appl
Sequence 12, Appl
Sequence 77, Appl
Sequence 1, Appli
Sequence 3112, Ap
Sequence 3112, Ap
GENERAL INFORMA
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Sequence 21, Appl
                                                                                                            February 11, 2004, 19:15:47; Search time 130.344 Seconds (without alignments) 4267.378 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/DS08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US00_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US00_PUBCOMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-138-888-21
US-10-138-888-9
US-10-138-888-10
US-10-138-888-11
US-10-138-888-12
US-10-138-888-77
US-09-981-606-1
US-09-764-877-3112
US-10-242-515-3112
US-10-138-888-1
US-10-138-888-3
US-10-138-888-5
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                                                                                                                                                                                                                                                                                          2449703 seqs, 1841816367 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
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seq length: 2000000000
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Maximum DB 8
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346, App
18770, Ap
4821, Ap
32571, A
2302, Ap
563, App
563, Appl
351, Appl
351, Appl
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17, Appl
10322, A
11044, A
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Sequence 21544, A
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Sequence 17,
Sequence 10
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COUNTRY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <a href="https://doi.org/10/138/888">UNAMPLICATION: <a href="https://doi.org/10/138/888">UNAMP
3. US-09-981-606-27

5. US-10-301-644-1

15. US-10-301-844-2

15. US-10-272-665-113

16. US-10-273-265-113

17. US-10-273-321-112

18. US-10-273-321-113

18. US-10-273-28-113

18. US-10-128-057-346

18. US-10-128-057-347

18. US-10-128-186-18770

18. US-10-128-188-18770

18. US-10-29-386-18770

18. US-10-29-386-5014

18. US-10-29-386-19081

US-09-964-761-21544
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STREET: 1155 Avenue of the Americas
CITY: New York
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ceredecaadaacadaaararace
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/10138888
; Publication No. US20030148972A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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Ruddy, David
                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                            /note= "normal or wild-type (unaffected)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: replace (328, "g")
CUTHER INDEMATION: /phenotype= "normal or wild-type (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 150; DB 13; Length 517; Pred. No. 1.8e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          genomic sequence surrounding variant for A4d1(G) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOCAGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                   REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
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Drayna, Dennis T.
Peder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
  04-APR-1996
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                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                         NAME: Brian M. Poissant
FILING DATE: 04-APR-19
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.3%;
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                         LOCATION:
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183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 1.517
OTHER INFORMATION: /note= "genomic sequence surrounding
variant for 24d1(A) allele corresponding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 13;
Pred. No. 1.8e-41;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                           NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence containing the HH gene
(SEQ ID NO:3)"
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KRY: allele
LOCATION: replace(328, "a")
OTHER INFORMATION: /phenoty
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  PAPELICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
FILING DATE: 23-MAX-1996
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1155 Avenue of the Americas
                                                                                                                                     121 CCTGGGGAAGAGCAGAGATATA¢GTNÇÇAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
Thomas, Winston J.
Prayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsychihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MCLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
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LOCATION:
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                                                                                                                                                                                                                                                          RESULT 4
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LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.3%; Score 150; DB 13; Length 1440; Best Local Similarity 99.3%; Pred. No. 2.4e-41; Matches 150; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: replace(1066, "g")
OCHER INVERMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION DATA:
RAPLICATION DATA:
APPLICATION DATA:
CALSON NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
                                 Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brian M. Poissant
REGISTATION UNDRER: 28,462
REFERENCE/DOCKET UNDRER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                               STREET: 1155 Avenue of the Americas
                                                                         NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: replace(414,
OTHER INFORMATION: /ph/
(unaffected)"
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TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 222..1268
           reuchihashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                          STATE: New York
COUNTRY: USA
                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (unaffected)"
/label= 24d2
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/label= 24d1 1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT ö

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981 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                         /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                          Length 1440;
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TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                          Score 150; DB 13;
Pred. No. 2.4e-41;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brian M. Poissant
REGISTRATION UNDMERE: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/834,497
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APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
                                                                                                                                                                                      /label= 24d2
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-138-888-12; Sequence 12, Application US/10138888; Publication No. US20030148972A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                           NAME/KEY: allele
LOCATION: replace(408,
OTHER INFORMATION: /phé
                              CDS
222..1268
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Matches 150; Conservative
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                                                     LOCATION:
           FEATURE:
NAME/KEY:
                                                                                                                                                                 (HH)
                                                                          FEATURE
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                                                                                                                                                                   1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                         Gaps
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0
                                                                             DB 13; Length 1440;
                                                                                                                       Indels
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ZIP: 10036-2711

COMPUTER READABLE PORD

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolff, Roger K.
INVENTION: Hereditary Hemochromatosis Gene
                                                                               Score 150; DB 13;
Pred. No. 2.4e-41;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
FILING DATE: 04-APR-1997
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                              121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-138-888-11; Sequence 11, Application US/10138888; Publication No. US20030148972A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   869-8864
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                                                                               99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Here
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                             Query Match
Best Local Similarity 99.3
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
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ATTORNEY/AGENT INFORMATION:

NAME: BITAIN M. POISSANT
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071
                           APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 2506
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                               LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%; Score 150; DB 13; Length 1440; 99.3%; Pred. No. 2.4e-41; ive 0; Mismatches 1; Indels 0.
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATE: US/10/138,888
FILING DATE: 02-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
THUChihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1041 CCTGGGAAGAGCAGAGATATACGTACCAGG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 77, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                    LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                     FEATURE
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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NAME/KEY: allele
LOCATION: replace(414, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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TITLE OF INVENTION: Mutations associated with iron disorders
FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
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1748 AAAGACGTATTGCCCAATGGGATGGACCTACCAGGGCTGGATAACCTTGGCTGTACC 1807
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PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PLING DATE: 2000-07-11
PRIOR PULING DATE: 2000-07-11
PRIOR PULING DATE: 2000-08-14
PRIOR PAPLICATION NUMBER: 60/225,758
PRIOR PAPLICATION NUMBER: 60/220,963
PRIOR PAPLICATION NUMBER: 60/217,496
PRIOR PAPLICATION NUMBER: 60/217,496
PRIOR PLING DATE: 2000-07-11
PRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-07-14
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Pred. No. 3.4e-41;
0; Mismatches 1; Indels 0
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Gnirke, Andreas
Ruddy, David
Tsuchashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1808 ceresesaasasesaasararaeseeeessa 1838
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-138-888-1
; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
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Best Local Similarity 99.3%;
Matches 150; Conservative
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                                                             0;
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                                                                                                          1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGCCAAGGAGTTCGAACCT
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                                                             Gaps
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US-09-764-877-3112

i Sequence 3112, Application US/09764877

i Patent No. US20020147140A1

i GENERAL INFORMATION:

i APPLICAMT: Rosen et al.

i TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PC005

CURRENT FILING DATE: 2001-01-17

CURRENT FILING DATE: 2001-01-17

Frior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

i SOFTWARE: PatentIn Ver. 2.0

i EENGTH: 5749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%; Score 150; DB 10; Length 5749;
99.3%; Pred. No. 3.4e-41;
live 0; Mismatches 1; Indels 0
       Score 150; DB 13; Length 2506; Pred. No. 2.7e-41;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCOOSCI.
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
                                                          1; Indels
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                                                          0; Mismatches
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COTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3112
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Publication No. US20040009488A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,629
PRIOR APPLICATION NUMBER: 60/180,629
     99.3%;
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Best Local Similarity 99.33
Matches 150; Conservative
                             Best Local Similarity 99.3
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
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     Query Match
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FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                     NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 28,462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                    (HH) protein"
/note= "No. US20030148972Almal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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Pred. No. 4e-41;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace(3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ghirke, Andreas
Ruddy, David
TRUCHIABHI, Zenta
WOLff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5809 CCTGGGGAAGAAGAGATATACGTGCCAGG 5839
                 PILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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APPLICATION NUMBER: US 08/834,497
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotyp
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Drayna, Dennis T.
                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 140..7319
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99.3%;
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Best Local Similarity
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APPLICANT: Thom
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5749 AAAGACGTATTGCCCCAATGGGGATGGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 5808
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99.3%; Score 150; DB 13; Length 10825;
Best Local Similarity 99.3%; Pred. No. 4e-41;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drayna, Dennis T.
Feder, John N.
Galirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brian M. Poissant
REGISTRATION WUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-884
OTHER INFORMATION: /product= "Heredii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccregegaagaccagagararaccrase 5839
                                                                                                                                                                                                                                                                      FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
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                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                       FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-138-888-5
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 140..7319
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5689 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 5748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

ATTORNEY/AGRYT INFORMATION:
NAME: Brian M. Poissant

REGISTRATION NUMBER: 8907-095-999

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 869-8864

OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing both the 24d1

and 24d2 mutations"
//ote- "Hereditary Hemochromatosis (HH) protein containing both the 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 150; DB 13; Length 10825; Pred. No. 4e-41; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
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NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
FLIASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5507..6023
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Best Local Similarity 99.3%;
Matches 150; Conservative
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LOCATION:
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US-10-138-888-79
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99.3%; Score 150; DB 13; Length 10825;
Best Local Similarity 99.3%; Pred. No. 4e-41;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                                                             COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFRWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFCATION SURNOWN>
PRIOR APPLICATION DATA:
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Teuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Hereditary Hemochromatosis (HH)
gene 24d2 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5809 ccreecaaadaccacacararacereccaee 5839
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/ACENT INFORMATION:
NAME: Brian M. Poissant
  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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US-10-138-888-7
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing the 24d7 mutation" /note= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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99.3%; Score 150; DB 13; Length 10825;
Best Local Similarity 99.3%; Pred. No. 4e-41;
Matches 150; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                CORRESPONDERS DEPLACES: 7, 79
CORRESPONDER ADDRESS:
CORRESPONDER ADDRESS:
COUNTRY: USA
CITY: New York
COUNTRY: USA
CIP: New York
COUNTRY: USA
CIP: New York
COUNTRY: USA
CIP: 10036-2711
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION NUMBER: US 08/834,497
FILING DATE: 04-MR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
                APPLICANT: Thomas, Winston J.

Prayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 24d7
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5507..6023
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GENERAL INFORMATION:
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Search completed: February 11, 2004, 22:07:08 Job time: 131.344 secs

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Sequence 5,
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Sequence 20,
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Sequence 3
Sequence 5
                                             Sequence Sequence
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APPLICANT: Rundell, Clark A.
APPLICANT: Vary, Calvin P.H.
TITLE OF INVENTION: STABLE ENCAPSULTATED REFERENCE
TITLE OF INVENTION: WICLEIC ACID AND METHOD OF MAKING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wood, Herron & Evans, L.L.P.
STREET: 2700 Carew Tower
CITY: Cincinnati
US-08-652-265-7

US-08-834-497A-1

US-08-834-497A-3

US-08-834-497A-7

US-09-503-444A-1

US-09-503-444A-3

US-09-503-444A-7

US-09-503-444A-7

US-09-503-444A-7

US-09-577-457-27

US-09-679-729-27

US-08-724-394A-21

US-08-724-394A-21

US-08-724-394A-21

US-08-724-394A-21

US-08-724-394A-21

US-08-914-372C-2

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3
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TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 360 base pairs
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 ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: huma
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MOLECULE TYPE:
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                                                                                                  February 11, 2004, 15:39:52; Search time 27.4222 Seconds (without alignments) 2430.473 Million cell updates/sec
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Sequence 4, Ap
Sequence 13, A
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/cgm2_6/ptodata/1/ina/5B_COMB.seq:*
/cgm2_6/ptodata/1/ina/6A_COMB.seq:*
/cgm2_6/ptodata/1/ina/RDTUS_COMB.seq:*
/cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-652-265-20
US-08-652-265-20
US-08-834-497A-21
US-09-503-444A-21
US-09-503-444A-21
US-09-503-444A-21
US-08-652-265-10
US-08-652-265-11
US-08-652-265-11
US-08-834-497A-10
US-08-834-497A-10
US-08-834-497A-10
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-09-503-444A-9
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-09-503-444A-11
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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243 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302
183 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 242
                                        61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACC
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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APPLICANT: TSUCHI
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STRANDEDNESS:
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US-08-632-673B-4
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US-08-632-673B-4
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STATE:
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DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
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Pred. No. 1.8e-43;
                      Score 150; DB 3; Length 360;
Pred. No. 1.6e-43;
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                                                                                                                                                                                                                                                        121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
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                                            Pred. No. 1.600; Mismatches
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APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08632673B Patent No. 5712098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0179:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drayna, Dennis T.
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Feder, John N.
TITLE OF INVENTION: HEREDITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchihashi, Zenta
Gnirke, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winston J.
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99.3<del>%</del>;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.33
Matches 150; Conservative
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                                        Best Local Similarity 99.3
Matches 150; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-632-673B-3
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APPLICANT:
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                          Query Match
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61 AAAGACGTATTGCCCAATGGGGATGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 150; DB 1; Length 517; Pred. No. 1.8e-43; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOWNSEND and TOWNSEND and CREW LLP
303 ccreegaadadcacadararacereccade 333
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CITY: San Francisco
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                                                                                                                                Sequence 4, Application US/08632673B Patent No. 5712098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
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Best Local Similarity 99.3%;
Matches 150; Conservative
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APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Feder, John N.
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Patent No. 6025130 GENERAL INFORMATION:
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APPLICANT:
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STATE: Ca
COUNTRY:
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                                                                                                                                                                                     APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Brady, David
APPLICANT: Wolff, Roger K.
APPLICANT: PEGET, John N.
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; L
1.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURALL.

PILING DATE: 16-Ar.
FILING DATE: 16-Ar.
FILING DATE: 16-Ar.
FILING DATE: 30.23
ATTORNEY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REPERENCE/DOCKEY NUMBER: 017957-000410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2401
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
TYPE: mucleic acid
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  303 CCTGGGGAAGACAGAGATATACGTACCAGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 150;
                                                                                                                           Sequence 13, Application US/08632673B Patent No. 5712098 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SPACE
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-632-673B-13
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                                                                                                                  US-08-632-673B-13
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STATE:
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RESULT 5 US-08-652-265-20 ; Sequence 20, Application US/08652265

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61 AAAGACGTATTGCCCCAATGGGGATTGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /phenotype= "normal or wild-type (unaffected)" /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
                                                     APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCTGGGGAAGAGCAGATATACGINCCAGG 151
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OTHER INFORMATION: /phenoty;
OTHER INFORMATION: (unaffect
Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.3
Matches 150; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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LOCATION: replace
                            Drayna,
                                                                                                                                                                                                                                                                                                                     USA
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LOCATION: 1.
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APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Truchihashi, Zenta
APPLICANT: Truchihashi, Zenta
APPLICANT: Will, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie F La-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic sequence surrounding variant for 24d1(G) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COKKESPUNDANCE ADDRESS:
COKKESPUNDANCE ADDRESS:
COKKESFORDANCE STATE:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONTYR: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 10-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 10-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: O4-APR-1996
      121 CCTGGGGAAGAGCAGATATACGTNCCAGG 151
                                                                    303 ceregedaadadeadaararaceraceade 333
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                                                                                                                                                                                                                         Sequence 20, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REPRENCE/DOCKET NUMBER: 8907
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: replace(328, "g")
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace (328, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 150; DB 3; Length 517; 99.3%; Pred. No. 1.8e-43; Live 0; Mismatches 1; Indels
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
FILING DATE: 23-MAY-1996
FILING DATE: 33-MAY-1996
TILING DATE: 33-MAY-1996
TILING DATE: 31-MAY-1996
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATTE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.33
Matches 150; Conservative
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LOCATION: 1...517
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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243 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 302
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                                                                                                                                                                                                                                                                                                                             /note= "genomic sequence surrounding
variant for 24d1(A) allele corresponding
to positions 5507-6023 of genomic
sequence containing the HH gene
(SEQ ID NO:3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /phenotype= "Hereditary Hemochromatosis
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99.3%; Score 150; DB 3; Length 517;
Best Local Similarity 99.3%; Pred. No. 1.8e-43;
Matches 150; Conservative 0; Mismatches 1; Indels
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC comparts:
COMPUTER: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= 24d1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      NAME/KEY:

LOCATION:
1..517
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
SEQUENCE CONTINER INFORMATION:
FEATURE:
NAME/KEY: allele
LOCATION: replace (328, "a")
OTHER INFORMATION:
                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                               LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   SEQUENCE CHARACTERISTICS:
                                                                                                                                                        linear
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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US-09-503-444A-20
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                                                                                                                                                    TOPOLOGY:
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APPLICANT: Drayna, Dennis T.
APPLICANT: Peder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Rucky, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Tsuchinashi, Tsuchina
                                                                                                                                                                                               Length 517;
                                                                                                                                                                                                                                                                          1; Indels
/phenotype= "normal or wild-type (unaffected)"
/label= 24dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION NUMBER: US 08/652,265
FILING DATE: 33-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION SATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
                                                                                                                                                                        uery Match 99.3%; Score 150; DB 3;
Best Local Similarity 99.3%; Pred. No. 1.8e-43;
Matches 150; Conservative 0; Mismatchem 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-834-497A-21
; Sequence 21. Application US/08834497A
; Patent No. 61403057
; GENERAL INFORMATTON:
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REGISTRATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
       ; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-834-497A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
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ZIP: 10036-2811
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TOPOLOGY: 11.
MOLECULE TYPE:
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US-08-652-265-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "normal or wild-type (unaffected) genomic sequence surrounding variant for 2441(g) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.3%; Score 150; DB 3; Length 517; Best Local Similarity 99.3%; Pred. No. 1.8e-43; Matches 150; Conservative 0; Mismatches 1; Indels
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Sequence 21, Application US/09503444A

GENERAL INFORMATION

APPLICANT: Thomas, Winston J.

APPLICANT: Peder, John N.

APPLICANT: Reddy, David

APPLICANT: Ruddy, David

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Weger K.

TILLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "normal or wild-type (unaffected)" /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 333
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1155 Avenue of the Americas
                 FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
APPLICATION NUMBER: 08/632,673
                                                                                                                              ATTORNAL PASSATE, BATAN MARE:
NAME: POISSANE, BATAN M.
REGISTRATION NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
TELEX: 66141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
STRANDENNESS: single
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OTHER INFORMATION: /phenotyr
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                       FILING DATE: 04-Apr-1996 ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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LOCATION: 1..517
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
LOCATION: replace(3)
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US-09-503-444A-21
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COUNTRY:

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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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variant for 24d1(A) allele corresponding
to positions 5507-6023 of genomic
sequence containing the HH gene
(SEQ ID NO:3)"
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NAME/KEY: allele
LOCATION: replace (328, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
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                                                                                                                                                                     FILING DATE: 14 Feb-200
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/62,265
FILING DATE: 23 May-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 16-Apr-1996
ATTORIEY/ABATI INFORMATION:
NAME: POISSANT INFORMATION:
REGISTRATION NUMBER: 28,462
REGISTRATION NUMBER: 212-790-9090
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
PILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08652265 Patent No. 6025130
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.3
Best Local Similarity 99.3
Matches 150; Conservative
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LOCATION: 1..517
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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61 AAAGACGTATTGCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 150; DB 3; Length 1440;
Pred. No. 2.7e-43;
0; Mismatches 1; Indels 0
                                                                                                                                           US-UD-032-20-10.

Detent No. 6025130

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

APPLICANT: Promas, Dennis T.

APPLICANT: Reder, John N.

APPLICANT: Ruddy, David

APPLICANT: Wolff, Roger K.

TITLE OF INVANTION: Hereditary Hemochromatosis Generalized For SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

CORRESPONDENCE ADDRESS: Townsend and Crew LLP

ATTER T TWO Embard and Townsend and Crew LLP

ATTER T TWO Embard and Townsend and Crew LLP

ATTER T TWO Embard and Townsend and Crew LLP

ATTER T TWO Embard and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ELDPSy disk
COMPUTER: ELDPSy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PATCHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,23
                                  1041 CCTGGGGAAGACAGATATACGTGCCAGG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCTGGGGAAGAGCAGATATACGTNCCAGG 151
121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGERENCE/DOCKET NUMBER: 1795
REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%;
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Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: TWO ENLANCE CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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LOCATION: 222..1268
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Best Local Similarity
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LOCATION: replace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Ca
                                                                                                                    RESULT 12
US-08-652-265-10
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(unaffected)"
/label= 24d1
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(unaffected)"
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(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING STSIEM: EV-LUGYMS-LOG
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILLING DATE: 23-MAY-1996
CLASSIFACATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: SMith, William M.
REGISTRATION NUMBER: 17957-000500
TELEBRACE/DOCKET NUMBER: 17957-000500
TELEBRACION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELEBRACION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELEBRACION NUMBER: 17957-000500
TELEBRACION NOW 9:
SEQUENCE (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: CDNA
MOLECULE TYPE: CDNA
                                APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     SSEE: Townsend and Townsend and Crew LLP
I: Two Embarcadero Center, Eighth Floor
San Francisco
: California
                                                                                                                                                                                                                                                                                                                              COUNTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION: (unaffected:
CTHER INFORMATION: (label= )."
US-08-652-265-9
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OTHER INFORMATION: /phenotyr
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= 2
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Best Local Similarity 99.3%;
Matches 150; Conservative 0
                    Dennis T.
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OTHER INFORMATION: /phem:
OTHER INFORMATION: (unafi
OTHER INFORMATION: /label
FBAUURE:
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222..1268
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                                                                                                                                                                                                                                                                                         STATE: Ca
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1041 CCTGGGGAAGAGCAGAGATATACGTGCCAGG 1071

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1041 CCTGGGGAAGAGCAGAGATATACGTACCAGG 1071

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981 AAAGACGTATTGCCCAATGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 1040
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99.3%; Score 150; DB 3; Length 1440;
Best Local Similarity 99.3%; Pred. No. 2.7e-43;
Matches 150; Conservative 0; Mismatches 1; Indels
                                                                                                          APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE MADDRESS:
ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCTGGGGAAGAGCAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRAION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LEAGHT: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 11, Application US/08652265 Patent No. 6025130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 222..1268
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                                                                Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas
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RESULT 13
US-08-652-265-11
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61 AAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCC 120
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                                                                                                                                            APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.3%; Score 150; DB 3;
Best Local Similarity 99.3%; Pred. No. 2.7e-43;
Matches 150; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                  ZIF. 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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               Sequence 12, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUCATION: replace (1066, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(408, "g")
                                                                                                         Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1440 base pairs
                                                                                                                        Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
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OTHER INFORMATION:
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LOCATION: replace
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                                                                                                         Drayna,
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LOCATION:
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JS-08-652-265-12
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921 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCT
                                                                                                                                                                                                                                                                                                                                                                     Score 150; DB 3; Length 1440; Pred. No. 2.7e-43;
PERTURE:

NAME/KEY: allale
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /unaffected)"
OTHER INFORMATION: /label= 24d7
FEATURE:
NAME/KEY: allale
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.3%;
Matches 150; Conservative
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       APPLICANT: Thomas, Winston J.
APPLICANT: Trayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsuddy, David
APPLICANT: Tsuddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: replace(408, "c")
OCHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
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COMPUTRY: New JOIK
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EMB PC COMPATIBLE
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: 04-APP-1997
FILING DATE: 04-APP-1997
FILING DATE: 03-MAY-1996
CLASSIFICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APP-1996
CLASSIFICATION STA
                                                                                                                       1041 CCTGGGGAAGAGCAGAATATACGTACCAGG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REPERENCE-DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDIRESS: single
                                                                                   121 CCTGGGGAAGAGCAGAGATATACGTNCCAGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                   Sequence 9, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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222..1268
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NAME/KEY:
LOCATION:
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US-08-834-497A-9
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Title: Perfect score:

Sequence:

OM nucleic

on:

Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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BF080089 230846 MA
BI339179 364041 MA
BG747345 602704818
AA217236 mu89205.r
BB851691 BB851691
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AKO89986 Mus muscu
AKO89561 Mus muscu
AKO8545 UL-M-CGOP
BF465475 UL-M-CGOP
BY745026 BY745026
                                                                                                               BB658165 BB858165

CASC6563 H4071807-

CASC6564 K044507-

BY159932 BY159932

BY20250 BY20250

BY319883 BY16250

BY319883 BY16880

BU746840 CH3#007_D

BU74680 CH3#007_D

BY196171 BY19617

BY206107 BY206107

BY10703 BY210730

BY17035 BY170353

BY18870 BY21670

BY198206 BY198206

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BY1982115 BY16870

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BY198206 BY198206
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AU132916 AU132916
CD960984 AGENCOURT
AL550540 AL550540
CD244248 AGENCOURT
CA454707 AGENCOURT
CA454707 AGENCOURT
BQ924511 AGENCOURT
BX415555 BX415555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM751283 544 bp mRNA linear EST 04-MAR-2002
K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5',
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 21C Frontier Korean EST Project 2001

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-44109
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 12 row: G column: 03
High quality sequence stop: 544.
             BI339179
BG747345
AA217236
BB851691
                                                                                                                                               BY159932
BY202250
BY319883
BU746849
BU746860
BY196171
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BY168570
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CH547869
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AK009581
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BQ924251
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BM751283
BM751283.1 GI:19080901
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  163.4
138.6
138.6
136.8
123
121.4
119.2
116.8
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102.6
102.6
102
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97.8
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AUTHORS
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BM751283
  AU279987 AU279987
CB162561 K-EST0223
BF883952 PM4-ET020
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                                                                  February 11, 2004, 14:16:30; Search time 1060.16 Seconds (without alignments) 6052.274 Million cell updates/sec
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                                                                                                                                 1 gttcacactctctgcactac......aaatcacaaccacagcaagg 264
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         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                    22781392 seqs, 12152238056 residues
                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                            US-09-981-606-27_COPY_4652_4915
264
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Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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99.4
85.2
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Score

Result No.

264 264 262.4 225

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Kim, Y.S.
21C Frontier Korean EST Project 2001
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143 c 168 g 124
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/clone_lib="89SNUGOI"
/clone_lib="89SNUGOI"
/note="Organ: Stomach; Vector: pME18-FL3; Site_l: XhoI;
/site_2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Sfil
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Supersoript II using Sfil
olgo-dT primer. After first strand synthesis, RNA was
degraded by NoOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with Sil and
cloned into DraIII - digested pME188-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOF' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
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100.0%; Pred. No. 6.7e-73;
ive 0; Mismatches 0;
                                                                                                                 /db_xref="taxon:9606"
/clone="S9SNU601-12-G03"
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cell line="SNU-601"
/lab_host="Top10F'"
                                                                                                                                                                                                          'tissue_type="Ascites"
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   Location/Qualifiers
                                                                                     /mol_type="mRNA"
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Contact: Takeo Isogai
Genemics Laboractory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-9975
Fax: 81-438-52-9975
Fax: 81-438-52-9976
Email: genomics@hri.co.jp
HRI human cDNA Project, Sugiyama,T.; Wakamatsu,A.; Irie,R.; Umezawa,A.; Furma,M.; Kusakari,S.; Hacka,J.; Ishii,K.; Yamamotco,J.; Isono,Y.; Saito,K.; Nakamura,Y.; Masuho,Y.; Nagai,K.; Isogai,T.
HRI human cDNA project; cDNA library construction & S'-end one pass sequencing: Helix Research Institute.

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1 (bases 1 to 52. Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sorea Research Institute of Bioscience & South Korea
Tel: +82-42-860-4470
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Pred. No. 6.8e-73;
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100.0%; Pred. No. c.
.. 0; Mismatches
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/Organizem: Trounc Bapticing
// mol type="mRNA"
// mol type="mRNA"
// db_xref="taxon:9606"
// dev stage="Adult"
// clone lib="ET0209"
// note="Organ: lung_tumor; Vector: puc18; Site 1: Sma1;
// Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Parent application No. 196,716 - Ludwig Institute for Cancer Research)
// profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                         Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4.ET0209-151200-003-407&t23=2000-12-15&t4=1)
High quality sequence start: 17
High quality sequence stop: 384.

Location/Qualifiers
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1 (bases 1 to 523)

Pahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush
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              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
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230846 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF080089
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 225; DB 10;
Pred. No. 1.4e-60;
0; Mismatches 0;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                          /lab host="Top10F'"
/clone lib="Li7N670205n1"
/clone lib="Li7N670205n1"
/note="Topgan: Liver; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: Not1; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 384)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., adsilva,W. Jr., Zago,M.A., Bordain,S., Costa,F.F., Nagai,M.A., Garvalho,A.F., Matenkuma,A., Baia,G.S., Simpson,D.H., Ernstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare.

Ennstein,A., Geoliveira,P.S., Reis,L.F., de Souza,S.J. and
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PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.
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Pred. No. 2.1e-72;
0; Mismatches 1; Indels 0;
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                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L17N670205n1-27-D07"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                    /organism="Homo sapiens"
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: D column: 07
High quality sequence stop: 535.
Location/Qualifiers
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Tel: 402 762 4366

Pax: 402 762 4390

Fax: 402 762 4390

Banail: maith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

VO.980904.e. Vector identified by cross_match with the -minscore 18

pcr PRimers
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I (bases 1 to 819)
NH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
//lab host="DH10B"
/clone_lib="WARC 2PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: Sal_Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pitultary, and placenta."
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.6%; Score 178.4; DB 12; Length
80.4%; Pred. No. 1.2e-45;
ive 0; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                         organism="Sus scrofa"
                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 100 row: C column: 24
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

vo.980904.e. Vector identified by cross_match with the -minscore 18

and -minmarch 12 options.

PCR PRIMERS

FORWARD: AGGAAACAGCTATGACGAT

BACKWARD: GTTTTCCGATCAGCAGG

BACKWARD: GTTTTCCGATCAGGAGG

BACKWARD: GTTTTCCGATCAGGAGG

BACKWARD: GTTTTCGAGTCAGAGG

Blate: 48 row: E column: 9

Seq primer: ATTTAGGTGACACTAATAG.
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Fabrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush
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/clone_lib="WARC_2PIG"
/note="Vector: pCMV_SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV_SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 175 c 152 g 93 t
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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Pred. No. 1.1e-45;
0; Mismatches 51; Indels 0;
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364041 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BI339179
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
                                                                                                                                                                                                                                                           Location/Qualifiers
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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/73 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                          /clone lib="Soares mouse lymph node NbMLN"
/note="Organ: lymph node; Vector: pI7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)

Hayatau, T., Azakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatau, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
'Y., Ito, M., Kawal, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
'A., Takahashi, F., Takaku, Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB851691 RIKEN full-length enriched, B16 F10Y cells Mus musculus cDNA clone G370002P09 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                  Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
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Pred. No. 6.2e-45;
0; Mismatches 55,
                                                                                                                                                                                                                                                      'tissue_type="lymph node"
                                                                                              organism="Mus musculus"
                                                                                                                                                                          'db xref="taxon:10090"
                                                                                                                                                                                                     'clone="IMAGE:652689"
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                                                                                                                                                                                                                                                                                 dev_stage="4 weeks"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                              sex="male"
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                                                                   1. .464
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                                                                                                                                                                                                                                                      /issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC_15"
/clone_lib="NH MGC_15"
/note="Corn" vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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mu89b05.rl Soares mouse lymph node NbMLN bus musculus cDNA clone
IMAGE:652689 5' similar to TR:G940354 G940354 CLASS I
HISTOCOMPATIBILITY ANTIGEN-LIKE PROTEIN: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Mamwalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Mooris,M., Tan,F., Underwood,K., Mooris,M., Tan,F., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 GACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGGAACTCCATGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 GITTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGGTCAGAGTCTGAAAGGGTGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 GAICACATGTTCACTGTTGACTTCTGGACTATTATGGAAAATCACAACCACAGGAAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 178; DB 10; Length 819;
100.0%; Pred. No. 1.9e-45;
ive 0; Mismatches 0; Indels
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1711 row: d column: 06
                                                                                                                                                          /organism="Homo sapiens"
                                                                              High quality sequence stop: 792.
                                                                                                                                                                                                                                         /clone="IMAGE:4857941"
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                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                            Location/Qualifiers
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Fax: 314 286 1810
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                            1 (bases 1 to 489)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                Mus musculus (house mouse)
  BE994943
BE994943.1 GI:10678689
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                                                                                                                                                                                                                                                                                                                                                                                                                  RIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                          Email: genome-readgac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carnindi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNs to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fyliwake,S., Inoue,K., Togawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, B16 F10x cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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    .481
    /organism="Mus musculus"

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/clone="G370002P09"
                                   Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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/dlone lib="XIH BNATE Red 52"
/dlone lib="XIH BNATE Red 52"
/note="Vector: pT7T3D-Pac"(Pharmacia) with a modified
polylinker; site 1: Not 1; Site 2: Eco RI; The
NIH BMAP Red 52 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
Uliversity School of Medicine
TAG SEQ=None found"
133 c 144 g 109 t
                                                                                                                                                                                                                                 oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine The following repetitive elements were found in this CDNA sequence: 1-31, >(CAG
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                                                                   6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, 20892-9643, USA
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Pred. No. 6.4e-45;
0; Mismatches 55; Indels
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/clone="UI-M-CG0p-bik-d-03-0-UI"
/lab_host="DH10B (Life Technologies)"
Contact: Chin, H
National Institute of Mental Health
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/organism="Mus musculus"
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/strain="C57BL/6J"
                                                                                                                                                                                                    Email: mEST@mail.nih.gov
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79.2%;
                                                                                                                                       Tel: 301 443 1706
Fax: 301 443 9890
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BE994943 1inear EST 29-APR-2002 UI-M-CG0p-bik-d-03-0-UI-81 NIH BMAP Ret4 S2 Mus musculus cDNA clone UI-M-CG0p-bik-d-03-0-UI 3', mRNA sequence.

DEFINITION

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Mus musculus
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TITLE
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Nuts musculus betazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 714)

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Quackenbush, J., Schini, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bult, C., Hume, D.A., Coobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, J.L., Konasaya, A., Kurachi, H., Yawaswa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawaswa, Y., Medzierski, R.M., King, B.L., Konasaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, H., Nagashima, T., Numata, K., Okido, T., Pavan, W., Jackson, I.J., Niki, P.A., Majlott, D.R., Maltais, L., Marchionni, L., Makeniel, L., Miki, Pescole, P. Rerovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Remple, C.A., Setou, R.D., Ramachandran, S., Ravasi, T., Red, J.C., Nang, Y., Red, J.C., Wang, Y., Hashala, K., Shinada, K., Shinada, X., Shinada, Y., Taylor, M., Shinada, K., Shinada, K., Taylor, M., Shinada, K., Shinada, Y., Wells, C., Whinshaw-Boris, A., Yanagisawa, K., Arakawa, T., Komo, H., Nakamura, M., Sakazume, N., Sarado, K., Marsha, T., Wani, K., Kawai, J., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conve
                                                                                                                                                                                                                                                                                                      EST 17-DEC-2002
243 ATCTGAGTCAGAGCCTGAAAGGTGGGACTACATGTTCATAGTAGACTTCTGGACCATCA 302
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URL:http://genome.gec.riken.go.jp,
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Hayaahida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S.,
Numazaki,R., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Sasaki,R., Ohno,M., Ohaato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                      303 TGGGCAACTATAACCACAGTAAGG 326
                                                                                         241 TGGAAAATCACAACCACAGCAAGG 264
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COMMENT

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genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Sxploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to Prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellsome Trust Centre for Molecular Mechanisms in Disease Wellcome assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="E430034J19"
/tissue_type="thymus"
/cell_type="thymic cells"
/clone_lib="RIKEN full-length enriched, 2 days neonate
thymus_thymic_cells (NOD)"
194 c 208 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GTTCACATTCTCTAAGATACCTCTTCATGGTGCCTCAGAGCCAGACCTCGGGCTGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 176; DB 14; Length 714; 79.2%; Pred. No. 7.7e-45; 1ve 0; Mismatches 55; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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High-efficiency full-length cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1719 bp
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1. .714
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/strain="NOD"
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JOURNAL

REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |db_xref="FANTOM DB:E430034J19"
|db_xref="taxon:10090"
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|dc_lone="taype="taymic cells"
|tissue_type="taymus"
|clone_lib="RIKEN full-length enriched mouse cDNA library"
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GWLTLAVAPGDETRFTCQVEHPGLDQPLTASWEPLQSQAMI IGIISGVTVCAIFLVGI
                                                        Fax:81-45-503-9216)
CONA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                       URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Pred. No. 1.2e-44;
0; Mismatches 55;
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7. .1173
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/strain="NOD"
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Matches
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

L Nature 420, 563-573 (2002)

6 (bases 1 to 1719)

7 Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashi, Y., Sahu, Y., Sodoo, H., Kowda, M., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowda, M., Katoh, H., Kawai, C., Sakayi, K., Sakazume, N., Sakai, K., Sakati, K., Sakati, M., Sakai, K., Sakazume, N., Sano, H., Sasaki, C., Sakazume, N., Sano, H., Sasaki, C., Sakazume, N., Sano, H., Sasaki, K., Shibata, K., Shinagawa, A., Shiraki, T., Sakazume, N., Sakazume, N., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                Itoh, M., Konno, H., Okazaki, Y., Muramateu, M., and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watshiki, M., Okazaki, Y., Muramatsu, M., Inoue, Y., Xira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), imboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GITCACAITCICIAAGAIACCICITICAIGGGIGCCICAGAGCCAGACCTCGGGCTGCCII 246
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,D., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Salto,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Yawamura,T., Yasunishi,A., Yoshida,K.,
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                                                                                                                                                                                                                                                         Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                      Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/db_xref="taxon:1099"
/db_host="bH10B (Life Technologies)"
/db_host="bH10B (Life Technologies)"
/clone lib="NH BMAP Ret4 S2"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP Ret4 S2 library is a subtracted library,
ultimately derived from mouse retina tissue library
ultimately derived from mouse retina tissue library
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.ulowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: Seq primer: M13 Forward
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TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 392)
Bonaldo,M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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strain="C57BL/6J"
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Fax: 301 443 9890
Email: mEST@mail.nib.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Characyt, Y., Euruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yammaka, I., Kiyosawa, H., Sajika, T., Malaaraki, Y., Nogami, A., Schonbach, C., Golobai, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matcher, C.F., Forrest, J. E., Cousins, S., Jalla, E., Dragani, T.A., Fletcher, C.F., Forrest, J. E., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kanai, A., Krazer, K.S., Gasterland, T., Marchiomi, L., McKenzie, E.D., Kanai, J. Hiokawa, N., Jackson, J. J., Jarvis, E.D., Kanai, A., Kurcchkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Mallais, L., Marchiomi, L., McKenzie, E.D., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pertovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Wangler, L., Wangler, K., Shinada, K., Sandelini, A., Schneider, C., Semple, C.A., Wangler, M., Sakazume, N., Sakazume,
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BY745026 RIKEN full-length enriched, bone marrow macrophage Musmussculus cDNA clone I830071K08 5', mRNA sequence.
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Pred. No. 1.2e-44;
0; Mismatches 56;
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Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new Genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length cDNA encyclopedia: real-time sequence Justering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                           Bmail: genome-res@gec.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Xoya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Nomura,K., Nomurazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramateu,M. and Hayashizaki,Y. Direct
                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Tissues were provided by David A. Hume ( Depts. of Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, bone marrow
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/clone="1830071K08"
  Contact: Yoshihide Hayashizaki
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 241 TGGAAAATCACAACCACAAGG 264

 Db
 444 TGGGCAACTATAACCACAGTAAGG 467

Search completed: February 11, 2004, 17:10:51 Job time : 1064.16 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

ВР ABK49917 standard; cDNA; 1317 (first entry) 15-JUL-2002 ABK49917; ABK4991

JNA encoding beta 2 microglobulin (beta2M)/HFE monochain.

iron absorption regulator; intracellular iron absorption; lung injury; haemolythomatosis; transfusion; thalassasemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR; brain tumour; cancer; oxidative stress disorder; tissue damage; vascular disease; Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia; inflammation; atherosclerosis; autoimmune disease, inflammatory condition; gene; ss.

Homo sapiens

"beta2M/HFE monochain" Location/Qualifiers 1..1317 /*tag= a /product= ' Key

WO200224929-A2

28-MAR-2002

24-SEP-2001; 2001WO-US29873

Haemochromatosis g Human colon specif Hereditary haemoch cDNA sequence enco

AAT96691 standard; cDNA; 1440 BP.

AAT9669.

AAT96691;

Laham N;

Rotem-Yehudar R,

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The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
malogue or active fragment), linked to alphal-alpha3 domains of human
HFE (a central regulator of iron absorption; undefined), or its analogue
or active fragment, by a flexible linker peptide, or a functional
HFE (a central regulator of iron absorption; undefined), or its analogue
or active fragment, by a flexible linker peptide, or a functional
consistence or all of (I). (I) is useful for reducing intracellular iron
absorption in patients having hereditary haemochromatcosis, transfersions,
consistence are preferably lymphocytes or leukocytes, across the blood-
brain barrier. (I) is further useful for treating brain tumour. (I)
consistence of the second or chronic infections, and for
consistence of the secular diseases, inflammation, atherosclerosis,
contoinmune diseases and inflammatory conditions. The monochain manifests
as a platform for drug delivery of therapeutic use for cancer,
contoinmune diseases and inflammatory conditions. The monochain manifests
specific characteristics advantageous for drug delivery systems. It is a
soluble, stable and fully conformed protein. It binds specifically to
transferrin receptor. (IfR) and therefore targets cells that over-express
this receptor. It is continuously internalised by the target cells, thus
enabling efficient drug delivery. It dissociates from the receptor in the
cells, minimising side effecte. It negatively regulates iron absorption,
reducing growth of undesired cells and preventing lymphocyte activation.
It is not diluted in the blood as is transferrin. It should not induce an
confundance response since it is a self non-polymeric protein and delivery of
arrian prevention mynesin mensor and any experience in the new page of the service of the se
                                                                                                                                                                                                                                                                           Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         natural TfR-binding protein. The present sequence represents the coding sequence of beta2m/HFB monochain.
                                                     UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 2; 77pp; English.
  22-SEP-2000; 2000US-234843P.
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                                                                                                                                                                                                                                                                                                                                                                    a linker peptide
                                                                                                                                                                                                                         P-PSDB; AAU80035
                                                                                                                                    Ehrlich R,
                                                     (UYRA-)
(MCIN/)
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Ouery Match
100.0%; Score 264; DB 24; Length 1317;
Best Local Similarity 100.0%; Pred. No. 9.2e-77;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;

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Gaps

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GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmaid-based cDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The following are claimed: a 10825 by genomic DNA sequence (1) (see following are claimed: a 10825 by genomic DNA sequence (1) (see following are claimed: a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants can an antibody produced using the peptide; a method to determine the presence or absence of the common HH gene mutation; an animal model for the HH disease; metal chelation

- useful for diagnosis

Hereditary haemochromatosis gene and variants - usefi and treatment of hereditary haemochromatosis disease

Disclosure, Fig 4; 115pp; English.

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"G to A substitution (24d1 mutation
associated with HH), results in Cys
Tyr substitution"
                                                                                                       g
"C to G substitution (24d2 mutation)
results in His to Asp substitution"
                                                                                                                                 h
"A to T substitution (24d7 variant)
results in Ser to Cys substitution"
                                        Hereditary haemochromatosis; metal toxicity; diagnosis;
                                                                                                                                                                                                                                                                                    Gnirke A, Ruddy D, Thomas WJ;
                           Hereditary haemochromatosis gene cDNA clone.
                                                gene therapy; prenatal screening; human; ss.
                                                                           Location/Qualifiers
222.1268
                                                                                                                                                                                                                                                                     (MERC-) MERCATOR GENETICS INC.
                                                                                                                                                                                                                                         96US-0652265.
96US-0630912.
96US-0632673.
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              14-APR-1998 (first entry)
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Tsuchihashi Z, Wolff
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P-PSDB; AAW36499.
                                                              Home sapiens
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16-APR-1996;
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Gaps

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alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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       New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hereditary hemochromatosis gene products or polypeptides, useful
                                                                                          The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed a having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for
                                                                                                                                                                                                                           100.0%; Score 264; DB 22; Length 1440; 100.0%; Pred. No. 9.6e-77;
                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                              Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
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                                                                                                                                                                                                                                                        0; Mismatches
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                                                               Disclosure, Fig 4; 108pp; English.
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96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                                        264; Conservative
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16-APR-1996;
23-MAY-1996;
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agents, T-cell differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or mitigation of iron overload, a method for screening potential therapeutic agents for activity in connection with HH disease, an antisense oligomucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligomucleotides or pairs of oligomucleotides covering a range of nucleotides from (I), (Ia) or their variants, useful for detecting a polymorphism in the HH gene. The invention also relates to methods for screening for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy,
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                                                                                                                                                                                                       Seguence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
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16-APR-1996;
23-MAY-1996;
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(BILL-) BILLUPS-ROTHENBERG INC
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                                                                                             The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cal differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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    treating hereditary hemochromatosis in a patient, and as a metal
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S65C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA sequence encoding a histocompatibility iron loading (HFE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; ss.
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                                                                                                                                                                                                                                  Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 other;
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"if this base is mutated to C,
protein contains the mutation
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                    chelation agent alleviating iron overload
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                                                          Disclosure; Fig 4; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C to G missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 160319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic
f
"if this base is mutated to C, then the
protein contains the mutation I105T, which
is associated with an iron overjoad disorder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 2-3; 55pp; English.
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Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
                                                                                                                                                                                          Detection of autosomal recessive disorder - particularly hereditary haemochromatosis, by detecting a mutation in the HC gene
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 other;
                                                                                                                                            (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                                                 Disclosure; Page -; 32pp; English.
                                            autosomal recessive disorder; ss
                                                                                                       97WO-AU00539
                                                                                                                      96AU-0002083
96AU-0001849
                                                                                                                                                            Cullen LM,
                     Haemochromatosis gene
                                                                                                                                                                          WPI; 1998-179064/16.
                                                                                                                      03-SEP-1996;
23-AUG-1996;
                                                           Homo sapiens
                                                                        WO9807884-A1
                                                                                                      22-AUG-1997;
                                                                                                                                                            Susfield F,
       10-JUL-1998
                                                                                       26-FEB-1998
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Powell LW;

Jazwinska EC,

This sequence represents the haemochromatosis (HC) gene. Mutations in this sequence are detected using the method of the invention. The method is for identifying an individual with hereditary haemochromatosis (HH) or a predisposition to develop HH or to genetically pass on HH to an offspring, comprising isolating a biological sample and amplifying a region of genomic DNA in the biological sample encompassing all or part of the DNA between markers D65255 and D65276, and detecting at least one homozygous or heterozygous mutation in a nucleotide within the region. The method can also be used for identifying an individual with an cutosomal recessive disorder (ARD) or predisposition to develop and/or genetically pass on an ARD to an offspring, comprises isolating a biological sample from the individual and screening genomic DNA in the sample for the presence of a homozygous or heterozygous mutation in a gene, the normal function of which, is required to prevent progression of the disorder. The method(s) can be used to identify individuals that are homozygous or heterozygous (carriers) for the mutation causing the ARD. Especially the method is used to diagnose HH or predisposition to HH by detecting a Cys282Tyr substitution. Individuals homozygous for this

0; Length 2727; Indels 100.0%; Score 264; DB 19; 100.0%; Pred. No. 1.2e-76; tive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 264; Conservative

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Indels

Query Match 100.0%; Score 264; DB 25; Best Local Similarity 100.0%; Pred. No. 1.7e-76; Matches 264; Conservative 0; Mismatches 0;

Length 5982;

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3521

3522 GCGGrGrGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3581

181 AGCIGAGICAGAGICTGAAAGGGIGGGAICACAIGITCACTGCIGACTICTGGACTATIA

121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC

61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3462 retricaacerricagecracerceaecracercricererrerargareaecre

3402 Gricacacretricacacracererreargacreereagagacerragreer 1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT

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3582 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTTATTA 3641

3642 TGGAAATCACAACCACAGCAAGG 3665

241 TGGAAAATCACAACCACAGGAAGG 264

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                                                                         298 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                   1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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(ABV93910-ABV94009) and proteins (ABP68360-ABP68435). The nucleic acids and proteins are useful for treating colon cancer and colon disorders, and diagnosing or monitoring the presence of colon disorders and metastases of colon cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer, and diagnosing or monitoring the presence of metastases of colon cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human colon specific nucleic acids
                                                                                                                                                                                               cytostatic; vaccine; gene therapy; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated colon-specific nucleic acid molecule, useful
                                                                                                                                                                     Human colon specific nucleic acid, SEQ ID 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 155-156; 216pp; English.
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                      TGGAAAATCACAACCAGGAAGG
TGGAAAATCACAACCACAGCAAGG
                                                                                         ₽.
                                                                                                                                                                                                             colon disorder; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                Ghosh MG,
                                                                                        ABV93934 standard; DNA; 5982
                                                                                                                                                                                                                                                                                                                  31-OCT-2001; 2001WO-US48414.
                                                                                                                                                                                                                                                                                                                                             31-OCT-2000; 2000US-244758P.
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                       (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-018928/01
                                                                                                                                                                                                                                                                                                                                                                                                Recipon H,
                                                                                                                                                                                                                                                              WO200277234-A2.
                                                                                                                                                                                                Human; colon;
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                           08-JAN-2003
                                                                                                                                                                                                                                                                                        03-OCT-2002
                                                                                                                ABV93934;
241
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                                                                                                                                                                                                                                                                                                                                                                                                Sun Y,
                                                                              ABV93934
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3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGGGTC 3881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3942 AGCTGAGTCTGAGAGTGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCCGTGTGGAGCCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 180
To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region of chromosome 6. A physical clone coverage was then generated extending from D6S265, which is a marker that is centromeric of HLA-A, in a telomeric direction through D6S276, a marker at which control of the allelic association was no longer observed. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a Cto A substitution that is present in casella in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary is tructure. The following are claimed: the HH genemic DNA (1), a structure. The following are claimed: the HH genemic DNA (1), a structure a cloning or expression vector; host cells; and 24d7 variants; a cloning or expression vector; host cells; a structure and 24d7, or a peptide of at least 56 amino acid cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of these; an antibody produced using the peptide; a method cesiques of the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or vivo or the mitigation of injury due to oxidative process or pairs of oligonucleotide directed against a transcriptional cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3762 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 100.0%; Score 264; DB 18; Length 10825; Local Similarity 100.0%; Pred. No. 2.2e-76; nes 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This genomic DNA sequence corresponds to the human gene whose mutated form is associated with hereditary haemochromatosis (HH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i
"G to A substitution (24d1 mutation
associated with HH), results in Cys to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
"C to G substitution (24d2 mutation)
results in His to Asp substitution"
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                                                                                                                                                                                                                                       Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.
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/note= "contains introns"
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Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                            Hereditary haemochromatosis gene.
                                                    AAT96690 standard; DNA; 10825 BP
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                                                                                                                                               14-APR-1998
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           RESULT 8
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Gaps

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P-PSDB; AAB36870.
   Homo sapiens.
                                                                 04-APR-1997;
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16-APR-1996;
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                       US6140305-A
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                                                                                                                                                                 Feder JN;
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                                                                                                                                                     Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                               New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 264; DB 22; Length 10825; 100.0%; Pred. No. 2.2e-76; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                     Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                        Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
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                                                                                                                                                    Gnirke A, Ruddy D,
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Matches 264; Conservative
                                                                                                                             (BIRA ) BIO-RAD LAB INC
                                                                                                                                                    Drayna DT,
                                                                                                                                                                                  2001-006341/01
                                                                                                                                                                                           P-PSDB; AAB36869
 Homo sapiens
                                                               04-APR-1997;
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16-APR-1996;
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                                                                                                                                                 Thomas WJ,
                                                                                                                                                              Feder JN;
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3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 3821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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                                                                                                                                                                                                                                  Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic DNA of a histocompatibility iron loading (HFE) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                               Gnirke A, Ruddy D,
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                                                  96US-0630912.
96US-0632673.
96US-0652265.
97US-0834497.
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WPI; 1998-240014/21
                                                                  Similarity
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                                                         Query Match
Best Local S:
Matches 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barton JC;
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                            iocation/Qualifiers
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/number= 6
10206..10637
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7995..9050
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9051..10205
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                                                                                    /number= 1
4652..4915
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          Homo sapiens
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4711
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4832 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4891
                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine butyrophilin; BT; human hereditary haemochromatosis; HPE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupuas Sjogren's syndrome; hypophosphatemia; type 1 soddum transport gene; ss.
                                                                                                                                                                                                                                                                    61 TGTTTGAAGCTTTGGGCTACGTGCATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
                                                                                                                                                                                                                              4652 GTTCACACTCTCCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                             GCCGTGTGGAGCCCCCGAACTCCATGGGTTTTCCAGTAGAATTTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                          1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hereditary haemochromatosis subregion from an unaffected individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes hereditary haemochromatosis gene
                                                                                                               Length 12146;
                                                                                                                                                     .
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mutation indicates the disorder or the genetic susceptibility disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop
                                                                             0 other;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas
                                                                             2474 C; 2911 G; 3378 T;
                                                                                                               100.0%; Score 264; DB 21;
100.0%; Pred. No. 2.3e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4892 TGGAAAATCACAACCACAGCAAGG 4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TGGAAAATCACAACCACAGGAAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lauer PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 8; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV57926 standard; DNA; 235033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0852495.
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                                                                           Sequence 12146 BP; 3383 A;
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                                                                                                                                                   264; Conservative
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Wolff RK;

Tsuchihashi Z,

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unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

C an providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of the haplotype or genotype where the presence or the HFB gene mutation in the genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present including and betyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type I sodium transport gene, and can can similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43208 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43388 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43328 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 43269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTGTGGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 43209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hereditary haemochromatosis subregion from an HH affected individual
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 264; DB 19; Length 235033; Best Local Similarity 100.0%; Pred. No. 7.8e-76; Matches 264; Conservative 0; Mismatches 0; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                          Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43148 TGGAAATCACAACCACAGCAAGG 43125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAAAATCACAACCACAGCAAGG 264
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Thomas WJ;

Ruddy DA,

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The products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis subregion from an hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

C above the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

C above the presence or absence of a haplotype or genotype where the presence or absence of the proportype or genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The the presence of the Present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present invention also describes BTF genes, which are homologues of the milk products for use in the diagnosis and treatment of HFB. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists of and antagonists of BT function. Also described are: (1) a Roket gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes while hard, he used for hymonlogues of a type 1 sodium transport gene, and can can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43338 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 43279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43278 rigiriridakiciririddacirakidriddakicakiriricdriciriririatardakidakir 43219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43158 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 43099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TGTTTGAAGCTTTGGGCTACGTGAACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCCGFGFGGGCCCCGAACTCCATGGGTTFCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                        editary haemochromatosis gene products - used to develop products the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                      present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 264; DB 19; Length 237326; 100.0%; Pred. No. 7.8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human hereditary hemochromatosis 24d2 mutation cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43098 TGGAAAATCACAACCACAGCAAGG 43075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for hypophosphatemia.
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                                                                                                                                                                                         Claim 1; Fig 9; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC68431 standard; DNA; 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 264; Conservative
                                           WPI; 1998-240014/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarly be
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                                                                                           Hereditary
                                                                                                                                           metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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#X#X####X#X#OOOOOOOOOOOOOOOOOOOOOOO
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31-OCT-2000,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537
                                                                                                                                                                                                                                                                                                                                        The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGATGAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                       RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                 New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                       Wolff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch
al Similarity 99.6%; Pred. No. 3.2e-76;
263; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                       ĸ,
                                                                                                                                                                       Tsuchihashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 other;
                                                                                                                                                                       Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561
                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 108pp; English.
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                                                                                                                                                                       Gnirke A,
                                                                         96US-0630912.
96US-0632673.
96US-0652265.
                                            97US-0834497.
                                                                                                                                        (BIRA ) BIO-RAD LAB INC
                                                                                                                                                                     Thomas WJ; Drayna DT,
Feder JN;
                                                                                                                                                                                                                     WPI; 2001-006341/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                          04-APR-1997;
                                                                         04-APR-1996;
16-APR-1996;
                                                                                                       23-MAY-1996;
              31-OCT-2000
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Human hereditary hemochromatosis 24d1/2 mutation cDNA

(first entry)

21-FEB-2001

AAC68432

BP

AAC68432 standard; DNA; 1440

HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss

Ното варіепв US6140305-A

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                                                                                                                                                                                                                                                                                                              The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                Wolff RK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                       New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
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                                                                                                                                                Tsuchihashi
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                                                                                                                                                Gnirke A, Ruddy D,
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e: 138.917 secs
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                                                     96US-0630912.
96US-0632673.
96US-0652265.
                          97US-0834497
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nes 263; Conservative
                                                                                                                   (BIRA ) BIO-RAD LAB INC
                                                                                                                                                 Thomas WJ, Drayna DT,
                                                                                                                                                                                           WPI; 2001-006341/01.
                          04-APR-1997;
                                                         04-APR-1996;
16-APR-1996;
                                                                                    23-MAY-1996;
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Sequence 9, Appli
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2: (ggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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7: (ggn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-138-888-10
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US-10-131-844-1
US-10-131-848-1
US-10-138-888-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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16 251.6 17 100 18 100 19 100 20 100								38			42		RESULT 1 US-10-189-889-9 Sequence 9, Application US/101 Publication No. USZO030148972A GENERAL INFORMATION: APPLICANT Thomas, Wins Feder, John Gnirke, Andr Ruddy, David THILE OF INVENTION: Her NUMBER OF SEQUENCES: 79 CORRESPONDENCE ADDRESS: ADDRESSE: Pennie STRRET: 1155 Avenu CITY: New York COMPUTER: New York COMPUTER: New York COMPUTER: New YORK COMPUTER: New YORK STATE: New YORK COMPUTER: New YORK COMPUTER: New YORK STATE: New YORK COMPUTER: New YORK COMPUTER: New YORK SOFFWARRE FILING DATE: 02-MA PRIOR APPLICATION DATA PRIOR APPLICATION DATA PRIOR APPLICATION DATA PRIOR APPLICATION DATA PRIOR APPLICATION OF APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER FILING DATE: 02-MA PRIOR APPLICATION NUMBER
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US-10-158-057-105 US-10-272-665-110 US-10-273-321-110 US-10-272-756-110 US-10-273-28-110 US-10-272-665-111	US-10-273-321-111 US-10-272-756-111 US-10-273-228-111	US-10-027-632-130689 US-10-027-632-130689 US-10-027-632-130689	US-10-027-632-130687 US-10-027-632-130688 US-10-027-632-130689	US-10-158-057-104	US-U9-814-353-20518 US-09-901-956-7	US-10-263-828-21 US-10-388-934-812	US-10-220-507-19 US-10-220-507-20	US-09-940-244-206	US-10-290-386-206	US-10-290-386-207	US-09-855-612-3	US-10-02/-632-209965 US-10-027-632-209965 US-10-191-803-28	on us/10138888 30148972A1 mas, Winston J. yna, Dennis T. rke, Andreas dy, Dennis T. rke, Andreas dy, David chihashi, Zenta ff, Roger K. TION: Hereditary Hemochromatosis Gene RENES: 9 ADDRESS: 15 Pennie & Edmonds LLP ADDRESS: 16 Pennie & Edmonds LLP ADRESS: 17 Avork W York W York M York M York M York M York M YOR SYSTEM: PC-DOS/MS-DOS PET Floppy disk IBM PC Compatible SYSTEM: PC-DOS/MS-DOS PATENIN Release #1.0, Version #1.30 ATION DATA: ON NUMBER: US/10/138,888 ATION: CURNOW- ION DATA: ON NUMBER: US 08/834,497 TE: 04-APR-1997 ON NUMBER: US 08/652,265
Sequence 105, App Sequence 110, App Sequence 110, App Sequence 110, App Sequence 110, App Sequence 111, App	Sequence 111, Sequence 111, Sequence 111,	Sequence 13068 Sequence 13068	Sequence 130688	Sequence 104, A	Sequence 7, App	Sequence 21, Ap Sequence 812, A	Sequence 19, Ap	Sequence 206, A	Sequence 206, A	Sequence 207, A		Sequence 209965 Sequence 209965 Sequence 28	eu og

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TYPE: nucleic acid
STRANDEDNESS: single
                                                                             NUMBER OF SEQUENCES: 79
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Best Local Similarity 100.
Matches 264; Conservative
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100.0%; Score 264; DB 13; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
              ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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US-10-138-888-10
Sequence 10, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                       CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                         allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                    FEATURE
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Drayna, Dennis T. Feder, John N. Gnirke, Andreas

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                                                                                                                                                                                                                  COUNTER READBALE FORM:

COMPUTER READBALE FORM:

MUDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: BASTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888

FILING DATE: 02-May-2002

CLASSIFICATION NUMBER: US/884,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 264; DB 13;
Pred. No. 1.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 28,462
REFERRICE/DOCKET NUMBER: 8907-095-999
TELECOMMULICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Scoll 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-MAY-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                          100.0%; Score 264; DB 14;
100.0%; Pred. No. 2.2e-83;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
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APPLICANT: Thomas, Winston J.
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                                                                                                                         FEATURE:

NAME/KEY: misc feature

LOCATION: (5885)...(5885)

OTHER INFORMATION: n=a, c, g or US-10-016-634A-25
                                                                                                       or
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                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (5780) .. (5780)
OTHER INFORMATION: n=a, c,
                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 264; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
  ORGANISM: Homo sapiens
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Sequence 25, Application US/10016634A

Sequence 25, Application US/10016634A

Sequence 25, Application US/10016634A

Sequence 25, Application US/10016634A

Publication No. US20020192666A1

GENERAL INFORMATION:
APPLICANT: Recipon, Herve
APPLICANT: Also, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Profite REPERENCE: DEX-0255

CURRENT APPLICATION NUMBER: US/10/016,634A

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION WUMBER: US 60/244,258

PRIOR APPLICATION OF SEQ ID NOS: 176

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 AGCTGAGTCAGACTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316
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478 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537
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                                                                                                                                                                                                                      US-09-981-606-1
; Sequence 1, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TILLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT FILING DATE: 2002-10-16
; PRIOR PAPLICATION NUMBER: US/09/981,606
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOSTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 264; DB 13; Length 2506; Best Local Similarity 100.0%; Pred. No. 1.5e-83; Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TGGAAATCACAACCACAGCAAGG 264
                                                                                241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                         538 TGGAAATCACAACCACAGCAAGG 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2506
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LENGTH: 5982
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CITY: New York

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                  NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPROMES: (212) 790-9090
TELEPROMES: (212) 790-9090
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                        (HH) protein"
/note= "No. US20030148972Almal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 264; DB 13; Length 10825; Best Local Similarity 100.0%; Pred. No. 2.9e-83; Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
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Feder, John N.

Gnirke, Andreas

Ruddy, David

Tsuchihashi, Zenta

Wolff, Roger K.

TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: replace(3878, "a")
OTHER INDEMATION: /phenotype
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4002 TGGAAAATCACAACCACAGGAAGG 4025
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US-10-138-888-3
; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 5507..6023
                                                                                                                                                                                                                                                           140..7319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (unaffected) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= 24d1
                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: U2-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497

APPLICATION NUMBER: US 08/652,265

APPLICATION NUMBER: US 08/652,265

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

APPLICATION NUMBER: US 08/650,912
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100.0%; Score 264; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.9e-83;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Hereditary Hemochromatosis (HH)
gene 24dl allele"
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TELEFAX: (212) 869-8864
OTHER INFORMATION: /produ
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STATE: New York
                         USA
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"ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
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Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
Wolff, Roger K.
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                                                                      TELEFAX: 650-493-5556
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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US-10-301-844-2/c
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Best Local (
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Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
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APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
GURENT APPLICATION NUMBER: U5/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
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APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 8907-0057-999
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ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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100.0%; Pred. No. 3(); ve 0; Mismatchel
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; Sequence 1, Application US/10301844
; Publication No. US20030100747A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brian M
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Best Local Similarity 100.
Matches 264; Conservative
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ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-981-606-27
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 12146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 235033;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <unversion of the compatible of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of the companies of 
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NAME: Poissant, Brian M
REGISTRATION UNDRER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 235033 base pairs
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APPLICATION NUMBER: US 08/630,912
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LOCATION: 222..1268
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: allele
NAME/KEY: replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
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ADDRESSE: Pernie & Edmonds LLP
STREET: LISS Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
CORPUTER: IBM PC compatible
CORPUTER: BEATON:
MEDIUM TYPE: RIOPPY disk
CORPUTER: BEATON:
CORPUTER: OF SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/138,888
FILING DATA:
FILING DATA:
FRIOR APPLICATION DATA:
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Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Freder, John N.
Galfer, Andreas
Ruddy, David
Tranchinabli, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237326 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43098 TGGAAAATCACAACCACAGCAAGG 43075
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TELEFAX: 650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 264; Conservative
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US-10-138-888-11
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                                                                                                                                                                                                                                                                                                                                                                                                   /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 1440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
FILING DATE: 04-APR-1996
ATTORNEY/AGRIT INFORMATION:
NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 9907-095-999
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.4%; Score 262.4; DB 1
Best Local Similarity 99.6%; Pred. No. 4.5e-83;
Matches 263; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11
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OTHER INFORMATION: /phenoty
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1 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                            Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, Bavid
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PXSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.4%; Score 262.4; DB 1
Best Local Similarity 99.6%; Pred. No. 4.5e-83;
Matches 263; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NATURER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
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SEQUENCE DESCRIPTION: SEQ ID NO: 77:
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OTHER INFORMATION: /phenoty
  538 TGGAAATCACAACCACAGCAAGG 561
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                 Sequence 77, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION:
                                                                                                                                                                                        APPLICANT: Thomas, Winston J. Drayna, Dennis T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 869-8864
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222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                             US-10-138-889-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 262.4; DB 13; Length 1440; 99.6%; Pred. No. 4.5e-83; cive 0; Mismatches 1; Indels 0;
                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138, 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brian M. Poissant
REGISTATION NUMBER: 28,462
REPERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype
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                                                                                                                                                                                        FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: replace (408, OTHER INFORMATION: /phe
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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222..1268
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MOLECULE TYPE: CDNA
FEATURE:
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Matches 263; Conservative
ZIP: 10036-2711
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Best_Local Similarity 99.6
Matches: 263; Conservative
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   NAME/KEY:
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US-10-138-888-7
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                                                                                    Query Match
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358 TGTTTGAAGCTTTGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGTGTC
                                                      TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC
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COMPUTER: ITEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-MAY-2002
CLASSIFICATION: CURNOWN-
PRIOR APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                             Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
OF INVENTION: Hereditary Hemochromatosis Gene
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomas, Winston J. Drayna, Dennis T.
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US-10-138-889-5
; GENERAL INFORMATION:
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                       298
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                                                                                                      Length 10825;
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Ruddy, David
Tsuchihashi, Zenta
Wolff, Woger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
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ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                      Score 262.4; DB 13;
Pred. No. 1.1e-82;
0; Mismatches 1;
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REFERRNCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-138-888-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dennis T.
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                                                                                                                                                                                                                                                                                                                            LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
TELEFAX: (212) 869-8864

OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing both the 24d1
and 24d2 mutations "
hote= "Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 99.4%; Score 262.4; DB 11 Local Similarity 99.6%; Pred. No. 1.1e-82; les 263; Conservative 0; Mismatches 1.
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                           /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Feder, John N.
                                                                                                                                                                                                 140..7319
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        allele
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                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
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US-10-138-888-79
                                                                                                                                                            FEATURE
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                                                                                                                                                                                                                                                                                                                                                                               (HH) pene 24d7 mutation" (HH) containing the 24d7 mutation" (HH) electronatosis (HH) allele" "Hereditary Hemochromatosis (HH) gene 24d7 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 262.4; DB 13; Length 10825; Pred. No. 1.1e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                         NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= 24d7
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype
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                       <Unknown>
02-May-2002
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140..7319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6%;
Matches 263; Conservative
                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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222..1268
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TOPOLOGY: 1i
MOLECULE TYPE:
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NAME/KEY:
LOCATION:
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LOCATION:
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  Sequence 9, Appli
Sequence 10, Appli
Sequence 9, Appli
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                                                                                                                                February 11, 2004, 15:14:45; Search time 33.2837 Seconds (without alignments) 3500.971 Million cell updates/sec
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Sequence 10, 7
Sequence 1, An
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Sequence 3, A
Sequence 1, A
Sequence 27, A
Sequence 27, A
Sequence 27, A
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Sequence
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-834-4497A-10
US-09-503-444A-9
US-09-679-7457-1
US-08-652-265-1
US-08-652-265-1
US-08-633-444A-1
US-08-834-497A-1
US-08-834-497A-1
US-09-503-444A-1
US-09-277-457-27
US-09-573-444A-3
US-09-679-27
US-08-679-27
US-08-724-394A-20
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US-08-724-394A-20
US-08-724-394A-20
US-08-724-494A-11
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US-08-652-265-7
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264
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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10825
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Perfect score:
Sequence:
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Maximum DB
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                                                                                                                                      Run on:
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28 222.4 99.4 10823 3 US-00-344.45-5 Sequence 5, Appli 202.4 99.4 10825 3 US-00-344.97-5 Sequence 5, Appli 202.4 99.4 10825 3 US-00-344.9-5 Sequence 5, Appli 202.4 99.4 10825 3 US-00-344.9-5 Sequence 5, Appli 202.4 99.4 10825 3 US-00-344.9-7 Sequence 5, Appli 202.4 99.4 10825 3 US-00-344.9-7 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 10825 3 US-00-344.9-93.4 Sequence 7, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.8 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4 108.9 Sequence 9, Appli 202.4 99.4
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NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPRENCENCE TOCKET: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IGGAAATCACAACCACAGGAAGG 264
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Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Garana, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY I
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 264; Conservative
                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 222..1268
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STATE: New York
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NAME/KEY:
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-652-265-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTTCAAGCCAGATGTGGCTGC 180
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| Patent No. 6025130
| GENERAL INFORMATION:
| APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T. APPLICANT: Beder, John N. APPLICANT: Reder, Andreas
| APPLICANT: Ruddy, David | APPLICANT: Teuchihashi, Zenta | APPLICANT: Teuchihashi, Zenta | APPLICANT: Wolff, Wager K. | TILLE OF INVENTION: Hereditary Hemochromatosis Gene
    /phenotype= "normal or wild-type (unaffected)"
/label= 24d2
                                                                                                                      /phenotype= "normal or wild-type (unaffected)"
/label= 24d7
                                                                                                                                                                              FEATURE:
NAME/KEY: allele
NAME/KEY: allele
COCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
US-08-652-265-9
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COUNTY: USA

ZIP: 94111-3834

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T: Two Embarcadero Center, Eighth Floor San Francisco California
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 264; DB 3;
100.0%; Pred. No. 2.5e-79;
iive 0; Mismatches 0;
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                                                                                                     LOCATION: replace (414, "a")
OTHER INPORMATION: /phenotyy
OTHER INFORMATION: (unaffect
OTHER INPORMATION: /label= &
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NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Matches 264; Conservative
    OTHER INFORMATION:
OTHER INFORMATION:
                                                                FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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US-08-652-265-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTTCAAGCCAGATGTGGCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                        1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                     ;
NAME/KEY: allele
LOCATION: replace(1066, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                        Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                              100.0%; Score 264; DB 3;
100.0%; Pred. No. 2.5e-79;
Live 0; Mismatches 0;
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537

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478 AGCTGAGTCAGAGTCTGAAAGGGTGGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 537
                                                                                                                                                                                                                                                                                                                                                                                                                       AFPLICANT: Feder, John N.
AFPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
STOPPERS SEE: Pennie E PA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER RALABLE FOLKER
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRACESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MA-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION 1514
PRIOR PATE OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OFFI
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                             241 TGGAAATCACAACCACAGCAAGG 264
                                                                                                                                                                                  538 TGGAAAATCACAACCACAGGAAGG 561
                                                                                                                                                                                                                                                                                       RESULT 4
10S-08-344-497A-10
1S-08-344-497A-10
1 Sequence 10, Application US/08834497A
1 Patent No. 6140305
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OTHER INFORMATION: /phenotype
OTHER INFORMATION:
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TELEX: 66141 PENNIE
INCOMPATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDENNES.
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NAME: Poissant, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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ZIP: 10036-2811
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 240
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Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
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              SYSTEM: Windows 95
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8907-0056-999
                                                      CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,497A

FILING DATE: 04-APR-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/652,265

FILING DATE: 13-MAY-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

CLASSIFICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION: 514

PRIOR APPLICATION: 514

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

CLASSIFICATION NUMBER: 28,462

REFERENCE CAPASITON NOWER: 28,462

REFERENCE CAPASITON NOWER: 28,495

TELENCOMMUNICATION INFORMATION:

TELENCOMMUNICATION INFORMATION:

TELENCOMMUNICATION NOW: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1440 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
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/label= 24d2
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OTHER INFORMATION: (unaffecto
OTHER INFORMATION: (unaffecto
OTHER INFORMATION: /label= 24
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LOCATION: replace(408, "c")
OTHER INFORMATION: (pasfect)
OTHER INFORMATION: (lasfect)
OTHER INFORMATION: /label=
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LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
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NAME/KEY: allele
                     OPERATING SYSTEM:
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61 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1440;
                                                                                                                                                                                                                                                                                                                  NAMEKEY: allele
LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /unaffected)"
OTHER INFORMATION: /label= 24d7
FEATURE:
NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
ADDRESSEVENERCE Bennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 264; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, Winston J.
APPLICANT: Drayra, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
                       TELEX: 66141
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1440 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
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     212-869-9741
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222..1268
                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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     TELEFAX:
                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                           GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGT
                                                                        Query Match 100.0%; Score 264; DB 3; Length 1440; Best Local Similarity 100.0%; Pred. No. 2.5e-79; Matches 264; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Feder, John N.
APPLICANT: Forlirke, Andreas
APPLICANT: Guirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
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PULIOR DATA.

APPLICATION NUMBER: 08/652,265
FILING DATE: 23 **May-1996
PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/632,673
FILING DATE: 16 **Apr-1996
PRIOR APPLICATION DATA.

APPLICATION NUMBER: 08/630,912
FILING DATE: 04 **Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSAIT, BRIAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Dennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TGGAAAATCACAACCACAGGAAGG 264
; OTHER INFORMATION: /label= 24d1
US-08-834-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09503444A, Patent No. 6228594, GENERAL INFORMATION:
APPLICANT: Thomas, Minston J. APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drayna, Dennis T.
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US-09-503-444A-9
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                                    APPLICANT: Application US/09277457
; Sequence 1, Application US/09277457
; Patent NO. 6355451
; GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry E.
; APPLICANT: Barda-Hirai, Ritsuko
APPLICANT: Barcon, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERRNCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
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; Sequence 1, Application US/09679729
; Sequence 1, Application US/09679729
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Barkon, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 24065-004 DIV
; CURRENT PRILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR PILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2506;
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color in Corp. in Spense mutation at nucleotide 314
US-09-277-457-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2506
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Best Local Similarity 100.
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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100.0%; Score 264; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.5e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                        PRIORALICATION:
PRIORATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
FILING DATE: 23-May-1996
PRIORATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIORATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, BRIAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/POCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-869-9741
                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
): 1155 Avenue of the Americas
New York
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CTHER INFORMATION: /phenotype= 'OTHER INFORMATION: /label= 24d1
US-09-503-444A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 222..1268
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                                                 New York
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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                      LOCATION: join(361...436, 3762...4025, 4235...4510, 5606..5881, LOCATION: 6040...6153, 7107...7147)
LOCATION: 6040...6153, 7107...7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6025130mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic
24d2(C)
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                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: normal or wild-type (unaffected) OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: normal or wild-type (unaffected) OTHER INFORMATION: sequence surrounding variant for OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions

OTHER INFORMATION: normal or wild-type (unaffected)

OTHER INFORMATION: sequence surrounding variant for

OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /phenotype= "normal or wild-type
(unaffected)"
/label= 24d2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /phenotype= "normal or wild-type
(unaffected)"
/label= 24d1
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100.0%; Pred. No. 6.2e-79;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace (5834, "g")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /unaffecte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: replace(3872, "c")
OTHER INPORMATION: (unafferorye
OTHER INFORMATION: (label= 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(3878, "a")
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (lnaffecte
OTHER INFORMATION: /label= 24
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Best Local Similarity 100.
Matches 264; Conservative
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LOCATION:
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                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 316
                                                                                                                                                                                                                     77 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT 136
                                                                                                                                                                                                                                                                                                                   137 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 196
                                                                                                                                                                                                                                                                                                                                                                                                                197 GCCGTGTGGAGCCCCGGAACTCCATGGGTTTCCAGTAGATTTTCAAGCCCAGATGTGGCTGC
                                                                                                                                                                       GITCACACTCICTGCACTACCICTICATGGGTGCCTCAGAGCAGGACCTTGGTC
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                                                                       Length 2506;
                                                                                                                         Indels
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) Patent No. 6025130
) GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Fuchihashi, Zenta
APPLICANT: Fuchihashi, Zenta
APPLICANT: Houghtinshi, Zenta
APPLICANT: Houghtinshi, Hereditary Hemochromatosis Gene
; OTHER INFORMATION: Missense mutation at nucleotide 314 US-09-679-729-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                         Query Match
100.0%; Score 264; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.2e-79;
Matches 264; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17957-000500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 TGGAAATCACAACCACAGGAAGG 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
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US-08-652-265-1
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/phenotype= "Hereditary Hemochromatosis
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COUNTY: New York
COUNTY: USA
ZIE: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FRANCE COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: FRASES for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4002 TGGAAATCACAACCACAGCAAGG 4025
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                             /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08834497A Patent No. 6140305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, Winston J. APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-652-265-3
                                                                                                                                              Similarity
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                                                                                                                       Query Match
                                                                                                                                                   Best Local
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis oTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)
OTHER INFORMATION: gene 24d1 allele"
FEATURE:
NAME/KEY: -
LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for oTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for OTHER INPORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Peder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TILLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSON'S
STRPPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPINY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 1814

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 17957-000500

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION STG 1D NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 10825 base pairs

TYPE: mucleic acid

TYPE: mucleic acid
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                             Sequence 3, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: replace(5834, "a")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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                           US-08-652-265-3
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                                                                                                                                                                                                                                                                                                                                          3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATGAGGAGTC 3881
                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                             61 IGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 120
                                                                                                                                                                                 3762 GTTCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
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                                                                                                                                      1 GITCACACTCTCTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCTTTCCT
                                                                       Gaps
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0
100.0%; Score 264; DB 3; Length 10825; 100.0%; Pred. No. 6.2e-79;
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APPLICANT: GAIRE, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITILE OF INVENTION:
                                                                   Indels
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3822 TGTTTGAAGCTTTGGGCTACGTGGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTC 3881
                                                                                  3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTTCAAGCCAGATGGCTGC
                                                121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 890'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEX: 650-493-556
TELEX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                 US-08-834-497A-3
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "No. 6140305mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d1(G) OTHER INFORMATION: allele (SEQ ID NO:20)"
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: footo.6153, 7107..7147)
LOCATION: footo.6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis oTHER INFORMATION: /note= "No. 6140305mal or wild-type (unafOTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: replace (3872, "c")
OTHER INFORMATION: (unaffected) "
OTHER INFORMATION: (unaffected) "
OTHER INFORMATION: (label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace (3878, "a")
OTHER INFORMATION: (label= 24d7
OTHER INFORMATION: (label= 24d7
FEATURE:
NAME/KEY: allele
LOCATION: replace (5834, "g")
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 264; Conservative 0; Mismatches 0;
                                                   8907-0056-999
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMULCATION INFORMATION:
TELEPHONE: 650-493-4935
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                       TOPOLOGY:
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3762 GITCACACICICIGCACIACCICITCAIGGGIGCCICAGAGCAGGACCIIGGICITICCI 3821

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3942 AGCTGAGTCTAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
181 AGCTGAGTCTGAAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Peder, John N.
APPLICANT: Peder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTOR: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRAEKSEQ for Windows 95
SOFTWARE: PARESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Pennie & Edmonds LLP
11155 Avenue of the Americas
New York
                                                                                                                                                                                           4002 resaharcacaacacacaass 4025
                                                                                                                            241 TGGAAATCACAACCACAGGAGG 264
                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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USA
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                                                                                                                   10036
ADDRESSEE:
                                                                 STATE: Ne COUNTRY: ZIP: 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3882 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941
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                  LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881, 10CATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"
OTHER INFORMATION: /note= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d1 allele"
NAME/KEY: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | LOCATION: replace(5834, "a")
| COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24dl
| US-08-834-497A-3
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 3852..3891
LOCATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 2462(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                      LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4002 TGGAAATCACAACCACAGCAAGG 4025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.8
Matches 264; Conservative
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                                                                                                                                                                                                                                                   140..7319
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
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(unaffected)
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6228594mal or wild-type (unafOTHER INFORMATION: hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d1(G)
allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 8907-0088-999;
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELERAX: 66141
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                           OPERATING SISTEM: WILDOWS 55
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/62,265
FILING DATE: 13-May 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
FILING DATE: 16-Apr-1996
PRIOR APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, BRIAN M.
REGISTRATION NUMBER: 28,462
BEGISTRATION NUMBER: 28,462
BEGISTRATION NUMBER: 28,462
Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTED:
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 5507..6023
OTHER INFORMATION: /r
OTHER INFORMATION: nc
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NAME/KEY: - 140..7319
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                                                   New York
: New York
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GCCGTGTGGAGCCCCGAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC
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                                                                                                                                                                                                                                                                                                                        100.0%; Score 264; DB 3; Length 10825; 100.0%; Pred. No. 6.2e-79; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-503-444A-3
is Sequence 3. Application US/09503444A
is Detent No. 6228594
is GENERAL INFORMATION:
is APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, John N.
APPLICANT: Gnirke, Andreas
is APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hareditary Hemochromatosis Gene
                                                        LOCATION: replace (3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /tabel= 24d7
FEATURE:
NAME/KEY: allele
LOCATION: replace (5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4002 regalalicaciaccacaccadade 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TGGAAAATCACAACCACAGCAAGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
/label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 99
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
OTHER INFORMATION:
                                        NAME/KEY: allele
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: USA
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                                                                                                                                                                                                                                                                             US-09-503-444A-1
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"

OTHER INFORMATION: /note= "Hereditary H~- OTHER INFORMATION: gene 24d1 all all the particle of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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Best Local Similarity 100.0%; Pred. No. 6.2e-79;
Matches 264; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: replace(5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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LOCATION: 3852..3891

LOCATION: /note= "start and stop positions for OTHER INFORMATION: qenomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
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OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: foroic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                         NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFRAX: 212-869-9741
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
APILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 24d1
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs TYPE: mucleic acid TYPE: "TECS: single
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3942 AGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTA 4001
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US-09-277-457-27

$ Sequence 27, Application US/09277457

$ Patent No. 6355425

$ GENERAL INFORMATION:

$ APPLICANT: Rothenberg, Barry E.

$ APPLICANT: Barcon, James C.

$ TILLE OF INVENTION: WITATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTATIONS ASSOCIATED WITH IRON DISORDERS

$ TILLE OF INVENTION: WUTATIONS ASSOCIATED WITH IRON DISORDERS

$ CURRENT APPLICATION WUMBER: US/09/277,457

$ CURRENT FILING DATE: 1999-03-26

$ NUMBER OF SEQ ID. NOS: 30

$ SEQ ID NO 27

$ IROTHER 12146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 264; DB 4; Length 12146; ; Pred. No. 6.5e-79; 0; Mismatches 0; Indels 0;
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                                              241 TGGAAAATCACAACCACAGGAAGG 264
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Best Local Similarity 100.0%;

Matches 264; Conservative 0
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CRGANISM: Homo Sapiens
US-09-277-457-27
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414.8
414.8
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ACCESSION
VERSION
KEYWORDS
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AR199263
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                                 February 11, 2004, 14:08:55; Search time 2119.64 Seconds (without alignments) 8376.333 Million cell updates/sec
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                                                                                                            5777422
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                       US-09-981-606-27_COPY_6494_6927
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Maximum Match 100%
Listing first 45 summaries
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                       OM nucleic
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Maximum DB
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AR117789 Sequence
AR117791 Sequence
AR149459 Sequence
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AL359892 Homo sapi
BD084121 Polymorph
AR036572 Sequence
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AF184234 Homo sapi
AR117790 Sequence
AR149460 Sequence
AR149460 Sequence
AR149462 Sequence
AF447807 Pan trogl
BD084122 Polymorph
AF331065 Homo sapi
AR117804 Sequence
AR149474 Sequence
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AF525359 Homo sapi
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AR109385 Homo sapi
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AR079408 Homo sapi
AY205604 Homo sapi
AJ249337 Homo sapi
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score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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Rothenberg, B.E., Sawada-Hirai, R. and Barton, J.C. Mutations associated with iron disorders
Patent: US 6355425-A 27 12-MAR-2002;
Location/Qualifiers
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                                      SUMMARIES
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AUTHORS
TITLE
JOURNAL
FEATURES
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240

6733

6793

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Bases I to 888)

Albig, W., Drabent, B., Burmester, N., Bode, C. and Doenecke, D.

The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is located in syntenic regions within the histone gene cluster 98208340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1999
                                                                                                                                                                                                                                                                                                       241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                                                                                                                                             GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
Goettingen, Biochemie und Molekulare Zellbiologie, Humboldtallee
23, Goettingen, FRG, 37073
Locating, Qualifiers
                                                                                                                                                                6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                                                                                                                                                                    6794 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
            TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGGATGGGACCTACCAGG
                                        6614 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG
                                                                             GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
                                                                                                6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGCTGGAGC
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gapes="HPPE"
function="iron metabolism"
/note="haemochromatosis candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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db_xref="GI:1890180"
db_xref="SWISS-PROT:Q30201"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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haemochromatosis; HFE gene.
Homo sapiens (human)
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Rothenberg.B.E., Sawada-Hirai,R. and Bart
Mutations associated with iron disorders
Patent: US 6509442-A 27 21-JAN-2003;
Location/Qualifiers
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Direct Submission
Submitted (04-DEC-1996) P. Gasparini, Servizio de Genetica Medica
IRCCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo
(FG), ITALY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
/map="6p22"
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H. sapiens HFE gene, exon 4 &
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       'translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
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4652. 4915
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0.0 181 GCTGGATAACCTTGGCTGACGAAGAGATATACGTGCCAGGTGGAGG	ARI17791 LOCUS DEFINITION Sequence 5 from patent US 6140305. ACCESSION ARI17791.0 GI:14098697 VERSION ARI17791.1 GI:14098697 KEYWORDS SOURCE ONGANISW Unknown. Unclassified. REFERENCE 1 (bases 1 to 10825) AUTHORS: Thomas W.J., Drayna, D.T., Feder,J.N., Gnirke,A., Ruddy,D., TSUChihashi,Z. and Wolff, R.K. TITLE Hereditary hemochromatosis gene products Unclassified. TSUCHIABS THOMAS W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., TSUChihashi,Z. and Wolff, R.K. TSUCHIABS THOMAS TO A STATUS TO A COURTNAL. TSUCHIHASHI,Z. and Wolff, R.K. TSUCHIHASH	rce NT Matc oca]	Db 56.06	181 5786 241 5846 301 361 5966
Best Local Similarity 99.8%; Pred. No. 1.86-129; Indels 0; Gaps 0; Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Gaps 1; Indels 0; Gaps 1; Indels 0; Gaps 0; Gaps 1; Indels 0; Gaps Qy 301 GCTGAGAAAATCTATTGGGGGTTGAGAGGGGTGATTATGGCAGTGAGA 360 Db 351 GCTGAGAAAATCTATTGGGGGTTGAGAGGGGTGAGGTAATTATGGCAGTGAGA 410 Cy 361 TGAGGATCTGCTCTTTGTTAGGGGATGGCCTGAGGGTGACTATAAGTTGC 420 Db 411 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGCCAATCAAAGGCTTTAACTTGC 420 Cy 421 TTTTCTGTTTTAG 434 Db 471 TTTTCTGTTTTAG 484	DNA linear	AUTHORS Tromas, W. L., Prayna, D.T., Feder, J.N., Ghirke, A., Kuddy, D., Truchihashi, Z. and Wolff, R. K. TITLE Hereditary hemochromatosis gene products JOURNAL Patent: US 6143305-A 1 31-OCT-2000; FEATURES Location/Qualifiers source 1. 10825 /organism="unknown" BASE COUNT 2998 a 2253 c 2648 g 2926 t	Query Match 99.6%; Score 432.4; DB 6; Length 10825; Best Local Similarity 99.8%; Pred. No. 2.5e-129; Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 TGCCTCCTTTGGTGACGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60 61 61 61 61 61 61 61 62 62 62 63 62 63 63 64	

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AL359892 193752 bp DNA linear HTG 13-JUN-2001
Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 134, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9864230.
---------------- Genome Center
Center: Sanger Centre
Center code: SC
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                               1 (bases 1 to 10825)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuchihashi, Z. and Wolff, R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 5 08-MAY-2001;
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                                                                                                                                                                                                                                                                                                 1 (bases 1 to 10825)
Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 1 08-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                              AR149459 10825 bp
Sequence 1 from patent US 6228594.
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AR149459.1
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                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; 108752; 100% of reads Sequencing vector: plasmid; 108752; 100% of reads Consensus quality: 183925 bases at least Q40 Consensus quality: 187703 bases at least Q30 Consensus quality: 187703 bases at least Q30 Consensus quality: 189658 bases at least Q30 Insert size: 192052; suu-of-contigs Insert size: 192052; suu-of-contigs Quality Coverage: 3.68x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1014 158659: contig of 4646 bp in length 16860 158759: gap of 100 bp 164235: contig of 5476 bp in length 1336 164335: gap of 100 bp 1336 184996: contig of 20661 bp in length 1997 185096: gap of 100 bp 18090; contig of 8656 bp in length 16004100/Qualifiers
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contig of 8504 bp in length
gap of 100 bp
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99.6%; Score 432.4; DB 2;
Best Local Similarity 99.8%; Pred. No. 3.3e-129;
Matches 433; Conservative 0; Mismatches 1;
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198209 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 198268
                                              PAT 29-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 246240)

1 (bases 1 to 246240)

Peder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Tsuchihashi,Z. and Wolff,R.K.

Megabase transcript map: novel sequences and antibodies thereto
Patent: US 587227-A 20 16-FEB-1999;

1. .246240
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Feder, J.N., Krommal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J., Tsuchihashi, Z. and Wolff, R.K.
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                                                  Unclassified.

[ bases 1 to 246240)

Peder., Unathan., Kronmal, G.Scott., Lauer, P.M., Ruddy, D.A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences and antibodies thereto
Patent: US 5872337-A 21 16-FEB-1999;
Location/Qualifiers
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Feder, J.Nathan., Kronmal, G.Scott., Lauer, P.M., Ruddy, D.A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences and antibodies th
Patent: US 587237-A 22 16-FEB-1999;
Location/Qualifiers
1. .246240
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Pred. No. 3.4e-129;
0; Mismatches 1;
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Sequence 22 from patent US 5872237.
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 GI:5953241
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Best Local Similarity 99.8%;
Matches 433; Conservative
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Unclassified.
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histone 2A-like protein
gene, RoRet gene, and
complete cds.
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Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L., Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N. Genome Res. 7 (5), 441-456 (1997)
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Buddy, D.A., Krommal, G.S., Iee, V.K., Mintier, G.A., Quintana, L.,
Domingo, R. Jr., Morer, N.C., Irrinke, A., McClelland, E., Fullan, A.,
Mapa, F.A., Morer, T., Thomas, W., Loeb, D.B., Harmon, C.,
Tsuchihashi, Z., Wolff, R.K., Schatzman, R.C. and Feder, J.N.
Direct Submission
Submitted (26-F8B-1997) Sequencing, Mercator Genetics, 4040
Campbell Avenue, Menlo Park, CA 94025, USA
Location/Qualifiers
1. 246282
| Jorganism="Homo sapiens"
| And Lype="genomic DNa"
| Ab_xref="taxon:9606"
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                                                                    Gaps
Length 246240;
                                                                    Indels
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Human hereditary haemochromatosis region,
gene, hereditary haemochromatosis (HLA-H);
sodium phosphate transporter (NPT3) gene,
U913281 GI:2088550
   DB 6;
   Score 432.4; DB 6;
Pred. No. 3.4e-129;
                                                                 0; Mismatches
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us-09-981-606-27_copy_6494_6927.rge

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/protein_id="AAM91950.1"
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/db_xref="G1:220949"
/db_xref="G1:220949"
/db_x
Heterozygote T->C mutation was detected at the intron 4 of the human hemachromatosis gene in an Africa American individual Unpublished 1913.

2 (bases 1 to 733)

Kutlar, F., Glendenning, M. and Kutlar, A.

Direct Submission

Submitted (28-JUN-2002) Medicine/Hematology-Oncology/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th street, AC-1000, Augusta, GA 30912, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ACCCAGGCCTGGATCAGCCCTCATTGTGATTTGTGACTGATGAGAGCCAGGA 300
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product="hereditary hemochromatosis protein precursor"
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/isolation source="African-American individual"
/db_xref="taxon:9606"
/chromosome="6"
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Pred. No. 6.1e-129;
0; Mismatches 2;
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gene="HFE"
note="HLA-H protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /_ccll_type="WBC"
<1. .>733
/gene="HFE"
/note="synonym: HLA-H"
join(<114. .389,548. .>661)
/gene="HFE"
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'replace="t"
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sex="female"
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Best Local Similarity 99.5%;
Matches 432; Conservative
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/gene="HFE"
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/gene="HFE"
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Homo sapiens hereditary hemochromatosis protein precursor (HFB)
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Kutlar,F., Glendenning,M. and Kutlar,A.
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Pred. No. 3.4e-129;
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Db 354 ACCCAGGCCTGGATCAGCCCTCATTGTGATTGTGACTGATGAGAGCCAGGA 413

Qy 301 GCTGAGAAAATCTATTGGGGGTTGAGAGGTGAGGTAATTATGGCAGTGAGA 360

Db 414 GCTGAGAAAATCTATTGGGGGTTGAGAGGTGCCTGAGGAGGTAATTATGGCAGTGAGA 473

Qy 361 TGAGGATCTGTTTGTTAGGGGATGGCTGAGGAGGTAATTATGGCAGTGAGA 473

Qy 421 TTTTCTGTTTTAG 434

Db 534 TTTTCTGTTTTAG 547

Search completed: February 11, 2004, 16:24:00

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SULT 1	
523554/C CUS	CB529554 729 bp mRNA linear EST 16-MAY-2003
FINITION	UI-H-FTZ-bjh-m-12-0-UI.81 NCI CGAP FTZ Homo sapiens cDNA clone
	UI-H-FT2-bjh-m-12-0-UI 3', mRNA sequence.
CESSION	CB529554
RSION	CB529554.1 GI:29390357
YWORDS	BST.
URCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
FERENCE	1 (bases 1 to 729)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
J	Tumor Gene Index
JOURNAL	Unpublished
MMENT	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
	Clone Distribution: Distribution information can be found at
	http://genome.uiowa.edu/distribution/cgap.html
	Seq primer: Ml3 FORWARD POLYA=Yes

CB529554 UI-H-FT2-BG747345 602704818 BE272926 601171213 BM723847 UI-E-E01-

CB529554 BG747345 BE272926 BM723847

10112

729 819 570 668

63.6 57.9 56.0 52.1

276 251.4 243 226

Description

Н

DB

Length

Query Match

Score

Result No.

ALIGNMENTS

BF038889

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BE272926 570 bp mRNA linear BST 13-JUL-2000 601171213F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3544803 5',
                                                                                                                                                                                                                                                            /lab host="NHIOB" (phage=resistant)"
/clone lib="NIH MGC 15"
/note="Corgan: colon; Vector: poTB7; Site_1: XhoI; Site_2:
BcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGGG (). Size-selected >SoObp for average
insert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
201 c 235 g 181 t
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM240 row: j column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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Pred. No. 5.2e-60;
0; Mismatches 1; Indels 2;
                                                                                                                                                                                                                                         tissue_type="adenocarcinoma cell line"
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http://image.llnl.gov
Plate: LLCM1711 row: d column:
High quality sequence stop: 792.
Location/Qualifiers
                                                                                                                                      sapiens"
                                                                                                                                 /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4857941"
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Tissue Procurement: DCTD/DTP
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Homo sapiens
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                                                                                                                                                                                                                                 /clone_libe="NCIC GAAP FT2"
/rote="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR I; Site_2: Not I;
NCI GAAP FT2 is a subtracted cDNA library constructed from a pol of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
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11 (bases 1 to 819)
NHI-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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602704818F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857941 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Best Local Similarity 100.0%; Pred. No. 5.7e-67;
Matches 276; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_LIB=UI-H-FT2
TAG_TISSUB=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCG"
211 c 165 g 202 t
                                                                                                                                                                               /dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                            tissue_type="Aveolar Macrophage"
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                                                                                                                                 clone="UI-H-FT2-bjh-m-12-0-UI"
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                                                    organism="Homo sapiens"
                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
     ocation/Qualifiers
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BG747345
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                                                                      /moi type="makna"
// db xref="taxon:9606"
/clone="IMAGE:1544803"
/tlssue type="renal cell adenocarcinoma"
/clone lib="NHT MGC_14"
/note="Organ: Kidney; Vector: pOTB7; Site_1: Xho1; Site_2:
EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/Xho1 sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synchesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 regareccaaegaerregaaceraaagaegrarrecccaaregegaregaecraecaeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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UI-E-EO1-aix-h-17-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aix-h-17-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           56.0%; Score 243; DB 10; Length 570; 100.0%; Pred. No. 1.1e-57; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coordinated Laboratory for Computational Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
                                                           organism="Homo sapiens"
High quality sequence stop: 566.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/ Organism= mRNA#
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B. Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
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cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Reverse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
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Pred. No. 7.1e-53;
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100.0%; Pred. No. /...
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/organism="Homo sapiens"
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Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                 TITLE
                Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 3301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.on). BAC end/ordestringframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 126\ {\rm c} 110 g 97\ {\rm t} 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="DHIOB"
/clone lib="RPCI-23"
/note="Corgan: Kidney/Brain, Vector: pBACe3.6; Site_1:
BCORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 TGCCTACTTTGGTGAAAGTGACTCGCCACTGGGGCCTCTACGGGGACCTCTCTAAGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 TGGATGCCAAAGATGTCAACCCCGAGAAGGTGCTACCTAACGGGGATGAGACCTATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 GCTGGCTAACAATGGCCGTGGCCCCTGGGGACGAGACAAGGTTCACCTGTCAAGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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0
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="RPCI-23-316A10"
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6 (Dases I to 171)
7 Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, M., Hirameto, K., Hiracaka, T., Hirozane, T.,
Hayashida, K., Hayatsu, M., Hirameto, K., Hiracane, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohosto, N.,
Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Tayaka, A., Shiraki, T.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 1719)
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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986 ACCCAGGCCTGGACCACCCTCTCACTGCCTCTTGGG 1021
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HTC; CAP trapper.
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseges.riken.go.jp, Pax:81-45-503-9216)
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                                                                                                                                                               CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
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Kawai, J. Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komo, H., Adachi, J., Fukuda, S., Arakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Yochiwa, H., Wagner, L., Mashio, T., Sakai, K., Okido, I., Furuno, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Tyo-oka, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Tyo-oka, K., Wangi, K.H., Weitz, C., Whittaker, C., Wilming, L., Whashizaki, Y., Yoshida, K., Haeegawa, Y., Kawaji, H., Kohtsuki, S.
HTC 05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  new genes
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
AK009581

Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length to EDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
21085660
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ligh-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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FIGURE 1.23-408722.TJ RPCI-23 Mus musculus genomic clone RPCI-23-408J22 AZ074871
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/lab host="DHIOB"
/clone lib="RPG1-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
BroRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Teegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/crderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
plttp://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 408 row: J column: 22
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 536)
                                                  1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fel: 301 838 0200
Indels
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69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 276
  0; Mismatches

    .536
    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/clone="RPCI-23-408J22"
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     207; Conservative
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Class: BAC ends.
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     Matches
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                                       Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Puruoo, M., Hanagaki, T., Hara, A., Ishii Y., Itamoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kato, H., Kawai, T., Miyazaki, A., Nishi, K., Suno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saaki, D., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sulucki, H., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Toya, C. Submission

Direct Submission

Submisted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Supplemention Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVDEWTINGNYNHSKYTKLGYVSESHILQVVIGCEVHEDNSTGGFWRYGYDGQDHLEF
CPKTLANWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLELGRGYLGQQV
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QGWLTLAVAPGDETFRFCQVEHPGLLQPLTASWEPLQSQAMIIGIISGVTVCAIFLVG
ILFLILRKRKASGGTWGGYVLTDCE"
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DLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWLHLSQSLKGWDYMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'tissue_type="tongue"
'clone_lib="RIKEN full-length enriched mouse cDNA library"
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/db_xref="MGI:1905246"
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/db_xref="GI:12844463"
/db_xref="MGI:109191"
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clone="2310032M04"
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/strain="C57BL/6J"
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1723
     Nature 420, 563-573 (2002)
6 (bases 1 to 1723)
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75.0%;
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Best Local Similarity
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          JOURNAL
                                  REFERENCE
                                                          AUTHORS
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/Globe="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoR1; Site 2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
135 c 112 g 108 t
lab_host="DH10B"
                                                                                                                                                                                                                                                                   34.3%;
al Similarity 73.4%;
204; Conservative (
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sites. The ligation products were transformed into electrocompetent cells (BRL Life Technologies). " , c 124~g~114~t~1 others
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Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: 376 row: C column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                   282
                                                                                                                                                                                                                                                                                                61 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 481)
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                                                                                                             35.5%; Score 154; DB 28; Length 536; 74.5%; Pred. No. 1.4e-32; cive 0; Mismatches 70; Indels
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Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ACCCAGGCCTGGATCAGCCCTCATTGTGATCTGGGGT 278
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/clone="RPCI-23-316C10"
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/strain="C57BL/6J"
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  EcoRI sites.
DH10B electro
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                                             149 C
                                                                                                                                       Best Local Similarity 74.5
Matches 207; Conservative
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SOURCE
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B1452668 831 bp mRNA linear EST 21-AUG-2001
603169877F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5249395 5',
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11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11629 row: j column: 20
High quality sequence stop: 818.
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                                                                                                                                                                   Gaps
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Score 148.8; DB 28; Length 481; Pred. No. 3.9e-31; 0; Mismatches 72; Indels 2;
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/clone="lhAdBs:524935s"
/tissue type="tumor, gross tissue"
/dev_stage="7 months"
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/mol_type="mRNA"
/strain="C57BL/63"
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Mus musculus
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ij

3; Gaps

493 226 433 286 373

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/clone="IMAGE:30376798"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="Diblo-Ton" A (T1 and T5 phage resistances)"
/clone_lib="NIH MGC 181"
/cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by linkert cogen). Note: this is a NIH MGC Library."

a 237 c 193 c lothers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.lln.gov

Plate: NDAM439 row: p column: 23

High quality sequence stop: 693.
                                                                                                                                                                                                                                                               CACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAA
                                                                                                                                                                                                                                                                                                                                    609 CACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTAAGGAGATCTCCCTGACCTGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plastic in the presence of 30% L929 supernatant."
1 171 c 163 g 144 t
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AGENCOURT 14098873 NIH MGC 181 Homo sapiens cDNA clone IMAGE:30376798 5', mRNA sequence.
                                                                                                                                   Length 611;
                                                                                                                                                        6.1e-14;
ches 95; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                   DB 14;
                                                                                                                                                                  Pred. No. 6.1e
0; Mismatches
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                                                                                                                                   88;
No. 6
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                                                                                                                                   tch 20.3%;
al Similarity 61.7%;
158; Conservative
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hote="Vector: pSPORTI; Site 1: NotI; Site 2: SalI;
hote="Vector: pSPORTI; Site 1: NotI; Site 2: SalI;
Library made from pools of polyA selected RNA, isolated at
different times post-infection (0 to 16 hrs) from African
swine fever virus (isolate Pretorisuskop/96/4) infected
swine macrophages. Macrophages were derived from
peripheral blood mononuclear cells cultured for 48 hrs on
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                 /clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 CAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 GTGGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TAACGGGGATGAGACCTATCAAGGCTGGCTGACATTGGCCGTGGCCCCTGGGGACGAGGC 121
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PO Box 848, Greenport, NY 11944-848, USA
PO ED 848, Greenport, NY 11944-848, USA
Fax: 631 323 3044
Email: jnellan@piadc.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim alt option. Vector identified by cross match v0.999329 and lucy v1.17p.
Seq primer: M13 Forward.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 611)
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                                                                                                                                                                                                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                 Score 105.2; DB 12; Length 831; Pred. No. 9.6e-19; 0; Mismatches 83; Indels 0;
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sn03_F06.f sn Sus scrofa cDNA 5', mRNA sequence.
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Plum Island Animal Disease Center
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/cell_type="macrophage"
/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9823"
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      /lab host="DH10B"
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                                                         3 CCTCCTTTGGTGAAGGTGACACCATCATGTGACCTCT---TCAGTGACCACTCTACGGTGT
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   Pred. No. 1.4e-13;
0; Mismatches 99; Indels
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Best Local Similarity 63.4%;
Matches 149; Conservative
   62.1%;
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                       172; Conservative
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Best Local Similarity
Matches 172; Conserv
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Sonstegard,T., Capuco,A.V., White,J., Van Tassell,C.P., Connor,E.E.,
Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and
Quackenbush,J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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/lab host="DH10B"
/clone_lib="BARC_SBOV"
/note="Vector: pCMV SDOYTE; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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                                                                                                 42 GTGACCACTCTACGGTGTCGGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGG
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                                                               Gape
                                                               Э;
                          Length 877;
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USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
TH: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE487497 1inear 176270 BARC 5BOV BOS taurus cDNA 5', mRNA sequence.
                                                             Indels
                                                             85;
                       Score 88; DB 14;
Pred. No. 7e-14;
0; Mismatches 85;
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/mol type="mRNA"
/db xref="taxon:9913"
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Plate: 138 row: G column: 4
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
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                        Query Match 20.3%;
Best Local Similarity 63.3%;
Matches 152; Conservative
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ABUUS947 752 bp DNA linear GSS 04-AUG-1997 Mouse genomic DNA, chromosome 17, clone cosmid 12.1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-JUL-1997) Masayasu Yoshino, U.T. Southwestern Medical
Center, HRM1, 5323 Harry Hines Blvd, Dallas, TX 75235-9050, U3A
(E-mail:YOSHINO@UTSW.SWHED EDU, Tel:214-648-5047, Fax:214-648-5453)
Location/Qualifiers
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Sciurognathi, Muridae, Murinae, Mus.
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196 c 198 g 192 t 5 others
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BAC clones from the H2-T region of the 129 mouse, Tlaf
Unpublished
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Pred. No. 2.1e-13;
0; Mismatches 83; Indels 3
443
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strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="17"
/clone="cosmid 12.1"
/haplotype="H2d"
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Mammalia; Eutheria; Rodentia;
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20.0%; Score 86.6; DB 10; Length 490;

Query Match

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/wol_type="mRNA"
/wol_type="mRNA"
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/tissue_type="RPE and Choroid"
/dev_stage="adult"
/dev_stage="adult"
/lab host="DH10B (Life Technologies) (Tl phage resistant)"
/clone_lib="UI-E-CII"
/lone="lib="UI-E-CII"
/note="Organ: eye; Vector: pT713-Pac (Pharmacia) with a modified polyllinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CII is a normalized CDNA library containing the following tissue(8): REE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6: 791-806, 1996. First strand CDNA synthesis was primed with an ollgo-df primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) B tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                EST 28-FEB-2002
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CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
303 TGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTCTTGGGAAAGAGCAGAGTTACAC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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                                                                                                 363 Argecardraracargaddacrigecraaddecrercaecerdagarddacraag 417
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UI-E-CII-afr-j-06-0-UI.rl UI-E-CI1 Homo sapiens CDNA clone
UI-E-CII-afr-j-06-0-UI 5', mRNA sequence.
                                                227 GTGCCAGGTGGAGCACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics
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TITLE
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Gaps

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19.6%; Score 85.2; DB 12; Length 467; 60.9%; Pred. No. 3.4e-13; Live 0; Mismatches 98; Indels 3;

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Query Match Best Local Similarity Matches 157; Conserv

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149
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vilnerary, anticonvulsant, antibacterial; antifungal; antiparasitic;
cardiant; gene therapy, cancer; immune disorder; cardiovascular disorder;
neurological disease, infection, human; secreted protein;
                       TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
                                                                                         GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing an iron disorder e.g. hemochromatosis or a genetic susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is used to diagnose an iron disorder
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100.0%; Pred. No. 1.2e-121;
ive 0; Mismatches 0;
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/number= 6
10206..10637
/*tag= m
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                                           /number= 3
6494..6769
/*tag= 9
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6928..7041
/*tag= i
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5401..6493
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/*tag= j
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Best Local Similarity 100.
Matches 434; Conservative
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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0246474.
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2000US-0226681.
2000US-0226868.
2000US-0227182.
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2000US-0228924.
2000US-0229287.
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2000US-0231242.
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20-OCT-2000;
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01-NOV-2000;
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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06-SEP-2000;
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08-SEP-2000;
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02-0CT-2000;
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02-0CT-2000;
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0246611.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249269.
17-NOV-2000; 2000US-0249269.
17-NOV-2000; 2000US-0249269.
17-NOV-2000; 2000US-0249269.
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17-NOV-2000; 2000US-0249269.
17-NOV-2000; 2000US-0251869.
0S-DEC-2000; 2000US-0251869.
0S-DEC-2000; 2000US-0251869.
0S-DEC-2000; 2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                              2000US-0254097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases such as wiral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.Wipo.int/pub/published_pot_sequences. Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.

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Disclosure; SEQ ID NO 3112; 321pp;
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2000US - 217486P
2000US - 219290P
2000US - 220964P
2000US - 224518P
2000US - 224518P
2000US - 225267P
2000US - 225268P
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2000US - 225757P
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2000US-229345P
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2000US-237037P.
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17-JAN-2001; 2001US-0764877
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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05-SEP-2000;
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Gene; se; musculoskeletal system antigen; cancer; metastasis;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
weardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
post-operative tissue repair; limb regeneration; neuronal growth;
well-related complex; chondrocyte growth; bone regeneration;
pariodental regeneration; tissue transport; bone graft; skin aging;
keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
weight; hair colour; ese colour; skin; percentage of adipose tissue;
pigmentation; commetic surgery; metabolism; biorhythm; caricadic rhythm;
depression; tendency for violence; pain; reproductive capability;
whormone level; endocrine level; appetite; libido; memory; stress;
storage capability; fat content; lipid content; protein content;
warbohydrate content; vitamin content; cofactor content;
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                                                                                                                                    TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 1664
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                                                                             Gaps
                                             Length 5749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding novel human musculoskeletal system antigen #2079
           Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                             Indels
                                           Score 432.4; DB 22;
Pred. No. 2.8e-121;
                                                                           0; Mismatches
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                                           99.6%;
99.8%;
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                                                                           Matches 433; Conservative
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                                                            Local Similarity
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                                             Query Match
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RESULT 3

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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
                                                                                                                                                                            English
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Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; ds.

Hereditary haemochromatosis gene

14-APR-1998 (first entry)

/*tag= a /note= "contains introns"

/number= 1 4026..4234

intron

Ω

137..3761 *tag=

intron

/number= 2

intron

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*tag=

cocation/Qualifiers

Homo sapiens

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conditions, such as, Alzheimer's disease, barkinson's disease, and Alzheimer's disease, parkinson's disease, and Alzheimer's stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sumburn by stimulating keratinocyte growth, prevents hair loss, since FGF family stimulating keratinocyte growth, prevents hair loss, since FGF family stimulating keratinocyte growth, prevents skin aging due to sumburn by stimulates activate hair-forming cells and promotes melanocyte growth, stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains crygans before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryons; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape colour, skin, percentage of adipose tissue, pigmentation, size, and shape colour, smill seate or physical state by influencing biorhythms, caricadic rhythms, depression, tenderny for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, late content, lipid, protenn, carbohydrate, vitamins, minerals, capabilities, metal state matalisms, minerals, coloured mannal state matalianal acceptage capabilities, or other mutritional components. This sequence encodes a novel human mutritional components. This sequence encodes a novel human
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regeneration; stimulates neuronal growth; can treat and prevent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculoskeletal system antigen.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                      neuronal damage occurring in certain disorders or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 432.4; DB 25; Length 5749; 99.8%; Pred. No. 2.8e-121; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
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Matches 433; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutated form is associated with hereditary haemochromatosis (HH). To identify this novel gene, allelic association patterns were determined between known markers and the HH locus in the HLA region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of chromosome 6. A physical clone coverage was then generated extending from D6S265, which is a marker that is centromeric of HLA-A, in a telomeric direction through D6S276, a marker at which
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/note= "G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
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                                                                                                                                                                                                                                                                                                            /*tag= g
/note= "C to G substitution (24d2 mutation)
                                                                                                                                                                                                                                                                                                                                                                    results in Ser to Cys substitution"
                                                                                                                                                                                                                                                                                                                             results in His to Asp substitution'
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/note= "A to T substitution (24d7 variant)
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96US-0632673.
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16-APR-1996;
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AAT96690 standard; DNA; 10825 BP.

RESULT 4
AAT96690
ID AAT90
XX
AC AAT90

AAT96690;

(first entry)

21-FEB-2001

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5785
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                                      critical cashociation was no longer observed. A single macarization disease. This comprises a G to A substitution that is present in disease. This comprises a G to A substitution that is present in disease. This comprises a G to A substitution that is present in the end affected chromosomes.

It results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary is tructure. The following are claimed: the Hi genomic DNA [1], a 1437 bp cDNA sequence (Ia) (see AAY36691) and their 24d1, 24d2 and 24d7, variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants contained product chosen from the HH gene product, its variants contained by the presence or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method for che common HH gene containing nor minal model for the HH disease; metal chelation agents, T-call differentiation factors and therapeutic agents for the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or the mitigation of injury due to oxidative process in vivo or criticense oligonucleotide directed against a transcriptional correction or pairs of oligonucleotide directed against a transcriptional correction mit directed against a range of nucleotides from the HH gene. The invention also relates to methods for greening the HH gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the HH gene. The invention also relates to moverable for HH homozygotes, to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapy, protein- and antibody-based therapeutics, and small molecule
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            allelic association was no longer observed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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patient, and as a metal
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                                                                                                                                                                                                                                                                                                                    Tsuchihashi Z,
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larity 99.8%; Pred. No. 3.5e-121;
Conservative 0; Mismatches 1;
                                                        HH; hereditary hemochromatosis; chelation agent; I-cell differentiation factor; iron overload; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               New hereditary hemochromatosis gene products for treating hereditary hemochromatosis in a chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                     Ruddy D,
                           Human hereditary hemochromatosis DNA
                                                                                                                                                                                                                                                                                                                       Gnirke A,
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96US-0652265.
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                                                                                                                                                                                                                                                                                                                     Thomas WJ, Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-006341/01.
P-PSDB; AAB36869.
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nes 433; Conserv
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23-MAY-1996;
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products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual unferced by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the EDNA or RNA from the presence of a haplotype or genotype where the presence of the HFE gene mutation in the genome of the individual. The HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protectin butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RORET gene which can be used to develop products for the study, diagnosis and
                                                                                                                                                                                            GCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; 88.
                               TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hereditary haemochromatosis subregion from an unaffected individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lauer PM, Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                          AAV57926 standard; DNA; 235033 BP.
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                                                                                                                                                                                                                                                                                                    6026 TTTTTCTGTTTTAG 6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US17658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-240014/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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01-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV57926;
                                                                                                                              9069
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                                                                                                                                                                                                                                                                                                                                                                                        AAV57926/c
                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 10825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%; Score 432.4; DB 22; Length
99.8%; Pred. No. 3.5e-121;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Human hereditary hemochromatosis 24d2 mutation DNA
                                                                                                                                                                                                                                                                                                                          HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ds.
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                                                                                                                                                      BP.
                                                                                                                                                      AAC68427 standard; DNA; 10825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0630912.
96US-0632673.
96US-0652265.
                               llarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0834497.
                                                                                                                                                                                                                                          21-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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23-MAY-1996;
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                                                                                                                                                                                                  AAC68427;
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                                              6026
        421
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GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                              The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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                                        New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                               Length 10825
                                                                                                                                                                                                                                                                                              0:
                                                                                                                                                                                                                                    Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                             / Match 99.3%; Score 430.8; DB 22; Local Similarity 99.5%; Pred. No. 1.1e-120; nes 432; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human hereditary hemochromatosis 24d1/2 mutation
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                                                                                                      Disclosure, Fig 3; 108pp; English
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WPI; 2001-006341/01.
P-PSDB; AAB36870.
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Matches
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      genes
                                                                                                                                                                                                                              41484 GGGCCTTGAACTACTACTACCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGGATAAGCAGAAA
                                                                                                                                                                                                                                                                                        41364 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGAATATACGTGCCAGGTGGAGC
                                                                                                                                                                           recercerregreaaggreacacarcargreaccrerreagreaccacreracggrere
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                                                                                                                                                                                                                                                                     TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
                                                                                                                                                                                                                                                                                                                             181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGATATACGTGCCAGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                        ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC
                                                                                                                                                  <u>TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC</u>
                                                                                                                      Gaps
                                                                                        DB 19; Length 235033;
   NPT4
                                                            235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 other;
                                                                                                                    0;
treatment of lupus and Sjogren's syndrome; and (2) NPT3 and which are homologues of a type 1 sodium transport gene, and similarly be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchibashi Z,
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation DNA
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T-cell differentiation factor; iron overload; ds
                                                                                       Score 432.4; DB 19
Pred. No. 1.1e-120;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 10825
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96US-0632673.
96US-0652265.
                                                                                       Query Match
Best Local Similarity 99.8%;
Matches 433; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-1996;
16-APR-1996;
23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Feder JN;
                                                                                                                                                                                                                                                                                                                                                                                          241
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                                                                                              Wolff RK;
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                                                                                                                                                                                                                             invention relates to hereditary hemochromatosis gene
                                                                                                                                                                                                                                                                                                                           DB 22; Length 10825;
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                                                                                                                                                                                                                                                                                                      Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;
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                                                                                               Tsuchihashi
                                                                                                                                                                                                                                                                                                                          Score 430.8; DB 22;
Pred. No. 1.1e-120;
0; Mismatches 2;
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                                                                                               Ruddy
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ID AAV57903 standard; DNA; 237326 BP.
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AC AAV57903;
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es 432; Conserv
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                                 04-APR-1996;
16-APR-1996;
23-MAY-1996;
              04-APR-1997;
                                                                                                  Thomas WJ,
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method to determine the presence or absence of the common hereditary haemochromatosis (HFB) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence of the haplotype genotype indicates the likely presence of the HFB gene mutation in the genome of the individual. The HFB gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFB. The present invention also describes BFF genes, which are homologues of the milk protein buttyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RORE gene and antagonists of develop products for the study, diagnosis and treatment of lupus and Siogran's syndrome, and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41496 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTC 41437
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                                                               Bovine butyrophilin; BT; human hereditary haemochromatosis; HFB; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
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Hereditary haemochromatosis subregion from an HH affected individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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Tsuchihashi Z, Wolff
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16-APR-1996;
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11316 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 41257
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                                        11256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGAGCCAGGA
                                                                                 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC
                        241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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a metal
                                                                                                                                                                                                                                                                                                                     Human hereditary hemochromatosis DNA used for mutation detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hereditary hemochromatosis gene products or polypeptides, for treating hereditary hemochromatosis in a patient, and as a chelation agent alleviating iron overload -
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llarity 99.8%; Pred. No. 8.4e-117;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; 88
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96US-0652265.
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                                                                                                                                                                                                                                                AAC68440 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006341/01
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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23-MAY-1996;
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                                                                                                                  361
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Best Local 9
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products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
               517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal
460 TGAGGATCTGCTCTTTGTTAGGGGGTGGGGGTGGCAATCAAAGGCTTTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolff
                                                                                                                                                                                                                                                                                                                                                          Human hereditary hemochromatosis DNA used for mutation detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to hereditary hemochromatosis gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 517 BP; 127 A; 120 C; 146 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chelation agent alleviating iron overload
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 6; 108pp; English.
                                                                                                                                                                               BP.
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96US-0632673.
96US-0652265.
                                                                                                                                                                               AAC68441 standard; DNA; 517
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Gaps

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9 90 120 150 180 210 240 330

us-09-981-606-27_copy_6494_6927.rng

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to encapsulate the mucleic acid, multiplying the cell to propagate the mucleic acid, inducing cell death without affecting the mucleic acid, and achieving a desired stability of the cell membrane for substantially matching the mucleic acid with the membrane stability of test cells. The reference nucleic acids are useful for molecular diagnosis and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iron absorption regulator; intracellular iron absorption; lung injury; haemochromatobis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR; brain tumour; cancer; oxidative stress disorder; tissue damage; vascular disease; inflammation; atherosclerosis; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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nucleic acid into a cell through its lipoprotein outer
                                                                                                                                                                                                                                                   Length 359;
                                                                                                                                                                                                                                                                                                 0; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                                                                                                                                                                                               Sequence 359 BP; 86 A; 91 C; 101 G; 81 T; 0 other;
                                                                                                                                                                                                                                             75.8%; Score 329; DB 20;
100.0%; Pred. No. 3.2e-90;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 329; Conserv
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                                                                                                                                                                                                                                                   219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hereditary hemochromatosis gene; encapsulate; lipoprotein outer membrane, membrane stability; test cell; molecular diagnosis; genetic testing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a nucleic acid sequence that is used as a reference sequence to exemplify the method of the invention. The specification describes a method for the biological preparation of a stably encapsulated reference nucleic acid for molecular diagnostic and genetic testing. The method comprises inserting a vector containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGGATCTGCTTTTTTTAGGGGATGGGCTGAGGGTGGCCAATCAAAGGCTTTAACTT 418
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                                                Gaps
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                                                ·;
DB 22; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary hemochromatosis gene target nucleic acid sequence.
                                                Indels
Score 414.8; DB 22,
Pred. No. 2.6e-116;
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                                                0; Mismatches
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95.6%;
                         99.58;
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                            Local Similarity
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                                                416;
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Query Match
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                                              Matches
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(first entry)

14-APR-1998

Laham N;

AAT96691;

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Example 2; Fig 2; 77pp; English.
     Ehrlich R, Rotem-Yehudar R,
          WPI; 2002-383192/41.
P-PSDB; AAU80035.
(MCIN/) MCINNIS P.
                           a linker peptide
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1073 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 1132 1013 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1072 953 recerectriegicaadesteacararcardicaecterreacreaecaecteraedester 1012 181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG 180 1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 60 Gaps 0 Score 277; DB 24; Length 1317; Pred. No. 3.8e-74; 0; Indels Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other; ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 277 Query Match 63.8%; Score 277; DB Best Local Similarity 100.0%; Pred. No. 3.8 Matches 277; Conservative 0; Mismatches 1133 241 121 61 a a ò Š 원 ò à

AAT96691 standard; cDNA; 1440 BP.

RESULT 15 AAT96691 ID AAT96

1193

This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based cDNA library following identification of the HH locus in the HLA region of chromosome . A single mutation (24d1) in the HH gene age to A substitution that majority of HH disease. This comprises a G to A substitution in the encoded protein (see AAM3649) at a chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a chromosome and in 4% of unaffected chromosomes. It results in a chromosome and in 4% of unaffected chromosomes. It results in a chromosome and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The critical disulphide bridge important for secondary structure. The collowing are claimed: a low sequence (I) (see AAT96690), the 1437 bp cDNA sequence (I) and their z4d1, z4d2 and 24d7 variants; a cloning or expression vector; host cells; a peptide product chosen from the HH gene product, its variants ceptide product chosen from the HH gene product of the common HH gene condensing the peptide; a method condetermine the presence or absence of the common HH gene mutation; an animal model for the HH disease; metal of agents for the mitigation of injury due to oxidative process in vivo or mitigation of iron overload; a method for screening potential Hereditary haemochromatosis gene and variants - useful for diagnosis and treatment of hereditary haemochromatosis disease i G to A substitution (24d1 mutation associated with HH), results in Cys to Tyr substitution" g "C to G substitution (24d2 mutation) results in His to Asp substitution" h "A to T substitution (24d7 variant) results in Ser to Cys substitution" Hereditary haemochromatosis; metal toxicity; diagnosis; Drayna DT, Feder JN, Gnirke A, Ruddy D, Thomas WJ; Tsuchihashi Z, Wolff RK; Hereditary haemochromatosis gene cDNA clone gene therapy; prenatal screening; human; ss Location/Qualifiers 222.1268 Disclosure, Fig 4; 115pp; English. (MERC-) MERCATOR GENETICS INC. 96US-0652265. 96US-0630912. 96US-0632673. 97WO-US06254 ď /*tag= 408 /*tag= /note= ' 1066 /*tag= /note= ' /*tag= /note= WPI; 1997-512743/47. 414 P-PSDB; AAW36499 04-APR-1997; 23-MAY-1996; 04-APR-1996; 16-APR-1996; sapiens WO9738137-A1 16-0CT-1997. variation mutation mutation Homo The invention relates to a soluble polypeptide (I) of beta 2

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

microglobulin (beta2m)/HFE monochain comprising human beta2m (or its

malogue or active fragment). Linked to alphal-alphal domains of human

HFE (a central regulator of iron absorption; undefined) or its analogue

or active fragment, by a flexible linker peptide, or a functional

ederivative or salt of (I). (I) is useful for reducing intracellular iron

absorption in patients having hereditary haemochromatosis, transfusions,

thalassaemias, haemolytic anaemia or chronic infections, and for

chain barrier. (I) is further useful for treating transfersin receptor

(TfR) which are preferably lymphocytes or leukocytes, across the blood
con an interpretating oxidative stress disorders resulting in

tissue damage e.g. vascular diseases, inflammation, atherosclerosis,

cutsimmune diseases and inflammatory of therapeutic use for cancer,

autoimmune diseases and inflammatory conditions. The monochain manifests

specific characteristics advantageous for drug delivery systems. It is a

specific characteristics advantageous for drug delivery systems. It is a

continuing efficiant drug delivery of therapeutic use for cancer,

cutoimmune diseases and inflammatory conditions. The monochain manifests

coluble, stable and fully conformed protein. It binds specifically or

cransferrin receptor (TfR) and therefore targets cells that over-express

this receptor. It is continuously internalised by the target cells, thus

cells, minimising side effects It negatively regulates iron absorption,

reducing growth of undesired cells and preventing lymphocyte activation.

cells, minimising side effects It negatively regulates iron absorption,

reducing yrowth of undesired cells and preventing lymphocyte activation.

cells, minimising is expected to overcome drug-resistance since it is a self non-polymeric protein and delivery of

charges via monochain is expected to overcome drug-resistance it is a self non-Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGG 1229 coding sequence of beta2m/HFE monochain.

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therapeutic agents for activity in connection with HH disease, an antisense oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above, and oligonucleotides CC or pairs of oligonucleotides covering a range of nucleotides from CC (I), (Ia) or their variants, useful for detecting a polymorphism in CC the HH gene. The invention also relates to methods for screening CC diagnosis, and therapies of HH disease, including gene therapy, CC diagnosis, and antibody-based therapeutics, and small molecule CC therapeutics.

XX Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 other;
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Search completed: February 11, 2004, 15:27:03 Job time : 226.083 sece

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February 11, 2004, 16:24:07; Search time 272.96 Seconds (without alignments) 5856.892 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                  2449703 seqs, 1841816367 residues
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		Description	Sequence 27, Appl	Sequence 3112, Ap	Sequence 3112, Ap	GENERAL INFORMA	GENERAL INFORMA	GENERAL INFORMA	Sequence 1, Appli	GENERAL INFORMA	GENERAL INFORMA	Sequence 2, Appli	Sequence 20, Appl	Sequence 21, Appl	Sequence 9, Appli	Sequence 11, Appl	Sequence 77, Appl
SUMMAKIES		qi	US-09-981-606-27	US-09-764-877-3112	US-10-242-515-3112	US-10-138-888-1	US-10-138-888-5	US-10-138-888-79	US-10-301-844-1	US-10-138-888-3	US-10-138-888-7	US-10-301-844-2	US-10-138-888-20	US-10-138-888-21	US-10-138-888-9	US-10-138-888-11	US-10-138-888-77
		DB	13	10	12	13	13	13	15	13	13	15	13	13	13	13	13
		Match Length DB	12146	5749	5749	10825	10825	10825	235033	10825	10825	237326	517	517	1440	1440	1440
	% Ouerv	Match	100.0	9.66	99.6	9.66	9.66	9.66	9.66	99.3	99.3	99.3	95.9	95.6	63.6	63.6	63.6
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	Sequence 5113, Ap Sequence 5114, Ap Sequence 351, App Sequence 383, App Sequence 19081, A Sequence 21544, A Sequence 21544, A Sequence 311, App Sequence 5325, Ap Sequence 5325, Ap Sequence 350, App Sequence 1870, App Sequence 1870, App Sequence 18710, A Sequence 18710, A
US-09-981-606-1 US-10-138-888-10 US-10-138-888-12 US-10-273-56-112 US-10-273-56-112 US-10-272-766-112 US-10-272-665-113 US-10-273-665-113 US-10-273-321-113 US-10-273-321-113 US-10-273-321-113 US-10-273-321-113 US-10-273-321-113 US-10-273-321-113 US-10-029-386-18154 US-10-029-386-18154 US-10-029-386-18154 US-10-029-386-18154 US-10-029-386-18154	US-09-880-107-3713 US-10-029-386-5014 US-10-029-386-5014 US-10-158-057-351 US-10-029-386-1981 US-09-864-761-21544 US-09-962-436-311 US-09-962-436-311 US-10-029-386-5325 US-10-158-057-350 US-10-158-057-350 US-10-029-386-18770 US-10-093-463-77 US-10-093-463-77
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                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 434; DB 13; Length 12146; 100.0%; Pred. No. 8.3e-139;
                                                                 APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
           ; Sequence 27, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 434; Conservative
                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  LENGTH: 12146
US-09-981-606-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies PILE REFERENCE: PC005C1
FILE REFERENCE: PC005C1
FRIOR PELICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
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PRIOR FILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PLICATION NUMBER: 60/225,447
PRIOR PLICATION NUMBER: 60/218,290
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99.6%; Score 432.4; DB 12;
Best Local Similarity 99.8%; Pred. No. 2.1e-138;
Matches 433; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                               Sequence 3112, Application US/10242515
Publication No. US20040009488A1
GENERAL INFORMATION:
                                       421 TTTTCTGTTTTAG 434
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ORGANISM: Homo sapiens
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US-10-242-515-3112
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3112
LENGTH: 5749
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Pred. No. 2.1e-138;
0; Mismatches 1;
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COTHER INFORMATION: n equals a,t,g, or US-09-764-877-3112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3112, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
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Best Local Similarity 99.8
Matches 433; Conservative
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US-09-764-877-3112
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                                                                                                                                                                                          Length 10825;
                                 NAME/KEY: allele
LOCATION: replace(5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
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                                                                                                                                                                                                DB 13;
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Pred. No. 2.8e-138;
0; Mismatches 1;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americae
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SEQUENCE DESCRIPTION: SEQ ID NO:
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
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Best Local Similarity 99.8%;
Matches 433; Conservative
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STATE: New York
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/label= 24d7
                  FEATURE
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                                     1905 GCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGTAATTATGGCAGTGAG 1964
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  GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=""No. US20030148972A1mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NOATER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                       Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                 US-10-138-888-1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
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                                                                                                                                                               TTTTTCTGTTTTAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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Orayna, Dennis T.

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Pred. No. 2.8e-138;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Hereditary Hemochromatosis (HH)
                                                                                                                                                                                                                                                               NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                  FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAX-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
FILING DATE: 02-May-2002
CLASSIFICATION: UDKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-138-888-5
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Best Local Similarity 99.8%;
Matches 433; Conservative
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.

RESULT 6 US-10-138-888-79

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OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                   Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 24d7 mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.6%; Score 432.4; DB 13
99.8%; Pred. No. 2.8e-138;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                              CURENT APPLICATION DATA:

CURENT APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIPICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREEF: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Hereditary Hemochromatosis
ne 24d7 allele"
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-138-888-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                          Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 869-8864
Feder, John N.
Gnirke, Andreas
Ruddy, David
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Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                           NUMBER OF SEQUENCES:
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41244 GCTGAGAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41185
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                                                                  GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA 120
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              41484 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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Frefer, John N.
Gnirke, Andreas
Ruddy, David
Tsucchinathi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
RELICON NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
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NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
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; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
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CORRESPONDENCE ADDRESS:
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TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785
                                                                                                                       300
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                                                                                                                   241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 235033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEO for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/301,844

FILING DATE: 20-No. US20030100747A1-2002

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 432.4; DB 15;
Pred. No. 1e-137;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPRONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMOCHROMATOSIS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 235033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10301844 Publication No. US20030100747A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 99.8%;
Matches 433; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           421 TTTTTCTGTTTTAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAAA 5725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
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                                           (HH) protein containing the 24d1
                                                                                                                                                                                                                                                                                                                     Score 430.8; DB 13; Length 10825;
Pred. No. 1e-137;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                      /note= "Hereditary Hemochromatosis (HH)
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                              LOCATION: 5507..6023
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-10-138-888-7
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                NAME/KEY: -
LOCATION: 140..7319
                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 99.5%;
Matches 432; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5666 egecerrenacracrececagnacarcarcarganetrasecrandereserandereserandes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace (5834, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis (HH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRA: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HI) protein containing both the 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.3%; Score 430.8; DB 13; Length Best Local Similarity 99.5%; Pred. No. 1e-137; Matches 432; Conservative 0; Mismatches 2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and 24d2 mutations"
//note="Hereditary Hemochromatosis (HH)
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/034,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                  APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5507..6023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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41136 TGAGGATCTGCTCTTTGTTAGGGGTGGGCTGGCGTGGCATCAAAGGCTTTAACTTGC 41077
                                          41316 GCTGGATAACCTTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTACCAGGTGGAGC 41257
                                                                                                                                41256 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 41197
                                                                                                                                                                                                                   41196 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 41137
    GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                                                                           GCTGAGAAAATCTATTGGGGGTTGAGGAGGAGTCCCTGAGGAGGTAATTATGGCAGTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TILE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/10138888
Publication No. US20030148972A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relefax: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TTTTTCTGTTTTAG 41063
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                                                                                                                                                                                                                                                                                                                                                    TITITICIGITITAG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-138-888-20
                                                                                          241
                                                                                                                                                                             301
                                                                                                                                                                                                                                                              361
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5906 GCTGAGAAATCTATTGGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 237326;
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OPERATING SYSTEM: Windows
SOFTWARE: FastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-No. US20030100747A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
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99.5%; Pred. No. 3.8e-137;
tive 0; Mismatches 2;
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERAK: 660-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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US-10-301-844-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 237326 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                            Sequence 2, Application US/10301844 Publication No. US20030100747A1 GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS
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US-10-301-844-2/c
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Matches 432;
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NAME/KEY: -
LOCATION: 1..517
OTHER INFORMATION:
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Best Local Similarity
Matches 416; Conserv
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                                                                                                                                    /note= "normal or wild-type (unaffected)
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                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(328, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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Gnirke, Andreas
Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
INVENTION: Hereditary Hemochromatosis Gene
                                                                     NAME/KET: -
LOCATION: 1.517
OTHER INFORMATION: /note= "normal or wilc
genomic sequence surrounding variant for
2441(G) allele corresponding to positions
5507-6023 of genomic sequence containing
the HH gene (SEQ ID NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.9%; Score 416.4; DB 13
99.8%; Pred. No. 2.6e-133;
tive 0; Mismatches 1;
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
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Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
MOLECULE TYPE: DNA (genomic)
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ZIP: 10036-2711
COMPUTER READABLE FORM:
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                                                                  NAME/KEY
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                                                                                                                                                                                                                                                                                                FEATURE
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US-10-138-888-21
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCCAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: replace(328, "a")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Variant for 24d1(A) allele corresponding to positions 5507-6023 of genomic sequence containing the HH gene (BEQ ID NO:3)"
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al Similarity 99.5%; Pred. No. 9.4e-133;
416; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 517 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                               1 TGCCTCCTTTGGTGAAGGTGACACATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                           NAME/KEY: allele
LOCATION: replace(1066, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type
             OTHER INFORMATION: /phenotype= "normal or wild-type
                                                                                                                                                                                                                                                                                 Length 1440;
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
WOLIF, ROGER K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 1.4e-84;
iive 0; Mismatches 0;
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
                                                                                                                                                                                     /label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
                                                                                                                                                                (unaffected) "
                                       (unaffected)
/label= 24d7
                                                                           FEATURE:
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400 GCTGAGAAATCTATTGGGGTTGAGAGGAGTCCTGAGGAGGTAATTATGGCAGTGAGA 459
                                                                  361 TGAGGATCTGCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 418
                                                                                                            460 TGAGGATCTGCTCTTTGTTAGGGGGGGCTGAGGGTGGCAATCAAAGGCTTTAACTT 517
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OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                                                                                                                                                                                                                                                                                                                                       Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: DE PC compatible
COMPUTER: DE PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/634,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

APPLICATION NUMBER: US 08/630,912

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allele
replace(414, "a")
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Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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                                                                                                                                                                                                                   Sequence 9, Application US/1013888
Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 869-8864
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222..1268
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-:
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= 24d2
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LOCATION:
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US-10-138-888-9
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Search completed: February 11, 2004, 21:02:46 Job time : 274.96 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGAACCTACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: replace(408, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
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Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6%; Score 276; DB 13; Best Local Similarity 100.0%; Pred. No. 1.4e-84; Matches 276; Conservative 0; Mismatches 0;
                                                                                 NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= 24d2
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                                                                                                                                                                                        LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           CDS
222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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1018 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGGCCTTGAACTACTCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCCAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            838 IGCCTCCTTIGGTGAAGGIGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: replace(414, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         °;
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COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1078 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGG 1113
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63.6%; Score 276; UB 13.7
Best Local Similarity 100.0%; Pred. No. 1.4e-84;
Matches 276; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brian M. Poissant
REGISTRATION WNDRBR: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            FILING DATE: 02-May-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
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STRANDEDNESS: single
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2004, 15:21:01 ; Search time 2489.59 Seconds (without alignments) 5781.298 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        using sw model
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seq length: 200000000
                                                                                                                                            nucleic search,
                                                                                                                                                                                                                 February 11,
                                  Copyright
                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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pna/US6006
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli Sequence 1, Appli Sequence 27, Appl Sequence 18070, A
Q1	100.0 12146 21 US-09-439-378-1 100.0 12146 21 US-09-439-378A-1 100.0 12146 43 US-09-981-606-27 99.6 2555 32 US-09-724-676-18070
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% Query Match Length DB	12146 12146 12146 2555
1	100.0 100.0 100.0 99.6
Score	434 434 434 432.4
Result No.	H 01 167 44

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Query Match
Best Local Similarity 100.
Matches 434; Conservative
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CRGANISM: Homo sapiens
US-09-439-378A-1
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US-09-439-378A-1
                                                        6614
                                                                                                            241
                      6554
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                                                                                                                          Sequence 11806, A Sequence 12922, A Sequence 1, Appli Sequence 1, Appli Sequence 1931, A Sequence 51931, A Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli GENERAL INFORMA GENERAL INFORMA
                          Sequence 3112, Ap
Sequence 3112, Ap
Sequence 3112, Ap
Sequence 112, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
GENERAL INFORMA
GENERAL INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-439-378-1
; Sequence 1, Application US/09439378
; Sequence 1, Application US/09439378
; GENERAL INFORMATION:
APPLICANT: London Health Sciences Centre
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS
; FILE REFERENCE: 4767-98/PAR
; CURRENT PILING DATE: 1999-11-15
; PRIOR PELING DATE: 1999-11-15
; PRIOR PILING DATE: 1999-12-1
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12146
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Sequence 20, Appl
Sequence 3, Appli
Sequence 20, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6494 TGCCTCCTTTGGTGAAGGTGACACATCATGACCTCTTCAGTGACCACTCTACGGTGTC 6553
  Sequence 18070, A
Sequence 18073, A
Sequence 18073, A
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Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                           Sequence 21, Appl
Sequence 18072, A
Sequence 18072, A
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US-09-764-877-3112
US-08-834-497-1
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US-10-138-888-7
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US-10-138-888-7
US-09-949-016-11806
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US-10-301-848-2
US-08-852-495G-2
US-08-834-497-20
US-08-891-256-3
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ORGANISM: Homo sapiens
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TILE OF INVENTION: METHOD FOR DIAGNOSIS OF HEREDITARY HEMOCHROMATOSIS
FILE REFERENCE: 4767-98/PAR
CURRENT APPLICATION NUMBER: US/09/439,378A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 2,272,410
PRIOR PELING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 8
SEG ID NO: 1
LENGRE: Patentin Ver. 2.1
LENGRH: 12146
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100.0%; Pred. No. 2.7e-117;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                         Sequence 27, Application US/09981606
GENERAL INFORMATION:
FAPPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders
FILE REFERENCE: 24065-004CON
CURRENT AFPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
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; Sequence 18070, Application US/09724676
; GENEAL INFORMATION:
; APPLICANT: Compugen LTD
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Matches 434; Conservative
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Pred. No. 4.7e-117;
0; Mismatches 1; Indels 0;
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TITLE OF INVENTION: Variants of alternative splicing FILE REFERRICE: 129181.4 Compagen CURRENT PEPLICEL: 129181.4 Compagen CURRENT FILING DAIR: US/09/724,676 CURRENT FILING DAIR: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 18070 LENGTH: 2555
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99.8%; Pred. No. 4.7e-117;
tive 0; Mismatches 1;
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TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181-4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ.ID NO 18070
LENGTH: 2555
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CNGANISM: Homo sapiens
US-09-724-676-18070
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US-09-724-676A-18070
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 4031 SOTWARE: Patentin Ver. 2.0 SEQ ID NO 3112 LEBRARY.
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC05PCT
CURRENT APPLICATION NUMBER: PCT/US01/01338
CURRENT FILING DATE: 2001-01-14
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 403.1
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 6.2e-117;
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CTHER INFORMATION: n equals a,t,g, or PCT-US01-01338-3112
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CTHER INFORMATION: n equals a,t,g,
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                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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PCT-US01-01338-3112
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           Length 5749;
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TITLE NO INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3112
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        Score 432.4; DB 2;
Pred. No. 6.2e-117;
0; Mismatches 1;
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COTHER INFORMATION: n equals a,t,g, or US-09-764-877-3112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3112, Application US/09764877; GENERAL INFORMATION:
        99.6%;
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Query Match
Best Local Similarity 99.8'
Matches 433; Conservative
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433; Conservative
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US-09-764-877-3112
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Matches 433,
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1665 GGGCCTTGAACTACTCCCCCAGAACAICACCATGAAGTGGCTGAAGGATAAGCAGCCAA 1724
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,497
FILING DATE: 04-APR-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, Winston J.
APPLICANT: Draya, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Houghy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08834497 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2025 Triricicitriras 2038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XY: USA
94111-3834
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CLASSIFICATION:
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                                                                                                                                                   241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGCCAGGA
                                                                                                1785 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
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Pred. No. 6.2e-117;
0; Mismatches 1;
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PRIOR PILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/19,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR PILING DATE: 2000-06-18
PRIOR PILING DATE: 2000-06-18
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3112, Application US/10242515; GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 433; Conservative (
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ORGANISM: Homo sapiens
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LENGTH: 5749
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5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG 5785
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                                                                                                                  GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGATATACGTGCCAGGTGGAGC
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APPLICANT: Peder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Truchashi, Zenta
APPLICANT: Truchashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPRY disk
MEDIUM TYPE: FIDPRY disk
MEDIUM TYPE: FIDPRY disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PRECHTIN Release #1.0, Version #1.30
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/834,497
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 2-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
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REFERENCE/DOCKET NUMBER: 017957-000520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
TELEFRAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08834497 GENERAL INFORMATION:
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: fnote= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele FATURE: CDTHER INFORMATION: cDNA (SEQ ID NO:9) " and flected) allele COATION: 3852.3891
LOCATION: 3852.3891
LOCATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: allele (SEQ ID NO:41) " allele (SEQ ID NO:41)" COTHER INFORMATION: allele (SEQ ID NO:41)" COTHER INFORMATION: normal or wild-type (unaffected) Genomic OTHER INFORMATION: allele (SEQ ID NO:20)" and the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of the convention of th
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "Normal or wild-type (unaffected) OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION; allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /phenotype= "normal or wild-type (unaffected)"
/label= 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /phenotype= "normal or wild-type
(unaffected)"
/label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /phenotype= "normal or wild-type (unaffected)"
/label= 24d1
REFERENCE/DOCKET NUMBER: 017957-000520US TELECOMUNIUS AT 17 TELEPHONE: (650) 326-2400
TELEPHONE: (650) 326-2422
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: replace (3872, "c")
OTHER INFORMATION: (phenotype=
OTHER INFORMATION: (unaffected
OTHER INFORMATION: /label= 24d;
FRATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: replace (3878, "a")
CTHER INFORMATION: /phenotype
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: /label= 24
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: replace(5834, "g")
OTHER INFORMATION: (unaffecte
OTHER INFORMATION: (label= 2.
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: -
LOCATION: 140..7319
                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                       TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-834-497-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC computatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-ARR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE:
ATTORNEY AGENT THORNATION:
ANDARY ACENT THORNATION:
ANDARY ACENT THORNATION:
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMOUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARROTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                       APPLICANT: Thomas, Winston J.
APPLICANT: Pader, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Williashi, Zenta
NUMBER OF SEQUENCES: 76
                                                                                                                                                                      Sequence 1, Application US/09497957
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
           6026 TTTTCTGTTTAG 6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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NAME/KEY:
                                                                                                                  RESULT 14
US-09-497-957-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5666 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAAA 5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGGACCTACCAGG 5785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5966 TGAGGATCTGCTCTTTGTTAGGGGGGGGGCTGAGGGTGGGCAATCAAAGGCTTTAACTTGC 6025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGCCAGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GCTGAGAAAATCTATTGGGGGTTGAGAGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TGAGGATCTGCTCTTTGTTAGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.6%; Score 432.4; DB 13; Length 10825; Best Local Similarity 99.8%; Pred. No. 7.6e-117; Matches 433; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..613, 7107..7147)
OTHER INFORMATION:
OTHER INFORMATION: mutation:
OTHER INFORMATION: mutation: mutation:
OTHER INFORMATION: gene 24d2 allele"
FEATURE:
NAME/KEY: -
NAME/KEY: -
NAME/KEY: -
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , LOUATION: replace(3872, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis; OTHER INFORMATION:
; OTHER INFORMATION: /label= 24d2
US-08-834-497-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 3852..3891
OCTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 5507..6023

UOCATION: COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

NAME/KEY: allele
LOCATION: replace(3872, "g")
                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 TTTTCTGTTTTAG 434
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LOCATION: join(361...436, 3762...4025, 4235...4510, 5606...5881, LOCATION: 6040...6153, 7107...7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Normal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
allele"
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OCTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele
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Sequence 5, Application US/09497957 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                  New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                         STATE: Ne
                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAATATACGTGCCAGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGATATACGTGCCAGGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGGATCTGCTTTTGTTAGGGGATGGGCTGAGGCTGCCAATCAAAGGCTTTAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
                                       NAME/KEY:

LOCATION: 3822..3891

LOCATION: JRCAMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2 (C) OTHER INFORMATION: allele (SEQ ID NO:41)"

FEATURE:
NAME/KEY: -
LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.6%; Score 432.4; DB 21; Length 10825; Best Local Similarity 99.8%; Pred. No. 7.6e-117; Matches 433; Conservative 0; Mismatches 1; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: replace(3872, "c")
OTHER INFORMATION: 'phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: allele
LOCATION: replace(3878, "a")
COTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: replace (5834, "g")
OTHER INFORMATION: 'phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2441
  CDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTCTGTTTTAG 434
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-497-957-1
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RESULT 15

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NAME/KRY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, COTHER INFORMATION: //product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation"

OTHER INFORMATION: //note= "Hereditary Hemochromatosis (HH) OTHER INFORMATION: gene 24d2 allele"
FEATURE:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Galirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: HERBITANY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
APPLICANT: WOLFF, ROSER K.
TITLE OF INVENTION: HERBITANY HEMOCHROMATOSIS GENE PRODUCTS
CORRESPONDENCE ADDRESS:
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LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant
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LOCATION: 140..7319
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/834,497

FILLING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILLING DATE: 13-APR-1996

FILLING DATE: 16-APR-1996

PRIOR APPLICATION NUMBER: US 08/632,673

FILLING DATE: 16-APR-1996

PRIOR APPLICATION DATA: 18-08/630,912

FILLING DATE: 04-APR-1996

ATTORNEY AGENT INFORMATION:

NAME: POISSANT, BRIAN M.

REGISTRATION NUMBER: 28,462

ATTORNEY AGENT INFORMATION:

NAME: POISSANT, BRIAN M.

REGISTRATION NUMBER: 28,462

TELEPHONE: 650-493-5556

TELEPHONE: 650-493-5556

TELEPHONE: 66141 PENNIE

INFORMATION FOR SEG ID NO: 5:

SEQUENCY TRANSCRERISTICS:
                                                                                                                                                                                                                                                                                                              1: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **OLECULE TYPE: DNA (genomic) FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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5606 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665
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      FEATURE:

NAME/KEY:

LOCATION: 5507..6023

CTHER INFORMATION: Genomic sequence surrounding variant of the INFORMATION: for 24d1(G) allele (SEQ ID NO:20) "
FEATURE:

NAME/KEY: allele

LOCATION: replace(3872, "g")

CTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis of the INFORMATION: /label= 24d2

US-09-497-957-5
                                                                                                                                                                                                                                                                                                                      Query Match
99.6%; Score 432.4; DB 21; Length 10825;
Best Local Similarity 99.8%; Pred. No. 7.6e-117;
Matches 433; Conservative 0; Mismatches 1; Indels 0;
OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
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ORGANISM: Homo Sapiens
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LENGTH: 12146
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            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-08-724-494A-3

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US-09-503-444A-3

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Maximum Match 100%
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Patent No. 6355425
GENERAL INFORMATION:
APPLICANT: Rothenberg, Barry B.
APPLICANT: Barron, James C.
TILLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS FILE REFERENCE: 10653/002001
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 100.0%; Pred. No. 1.1e-141;
14; Conservative 0; Mismatches 0;
US-08-652-265-9

US-08-652-265-11

US-08-834-497A-19

US-08-834-497A-19

US-09-503-444A-11

US-09-507-445A-11

US-09-679-729-1

US-08-652-265-10

US-08-652-265-10

US-08-834-497A-12

US-08-834-497A-12

US-08-834-447A-12

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3
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6854 TGAGGATCTGTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6674 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGG 6733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6734 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGGCCAGGA 6793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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                                                                                                                                                                            Sequence 27, Application US/09679729

Sequence 27, Application US/09679729

Setent No. 6509442

GENERAL INFORMATION:

APPLICANT: Rothenberg, Barry E.

APPLICANT: Barton, James C.

TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS

FILE REFERENCE: 24065-004 DIV

CURRENT APPLICATION NUMBER: US/09/679,729

CURRENT PILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: 09/277,457

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE FESTER FASTER FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 434; DB 4; Length 12146;
100.0%; Pred. No. 1.1e-141;
Live 0; Mismatches 0; Indels 0;
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Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                 6927
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Best Local Similarity 100.
Matches 434; Conservative
                                         421 TTTTTCTGTTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 27
LENGTH: 12146
                                                                                                                                                                 US-09-679-729-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-679-729-27
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/note= "No. 6025130mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
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OTHER INFORMATION: aller-
OTHER INFORMATION: differed and stop positions for OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: cDNA (SEQ ID NO:9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 3852..3891
LOCATION: Anote= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) POTHER INFORMATION: allele (SEQ ID NO:41)"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "start and stop positions for
normal or wild-type (unaffected) genomic
sequence surrounding variant for 24d1(G)
allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..56
LOCATION: join(361..436, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
COMPUTER HILDS BE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP FC.compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION IN-1996
ATTORNEY SMETH INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,223
REFERENCY DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENDERAX: 10825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: replace(3872, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d2
APPLICANT: Feder, John N.
APPLICANT: Grairke, Andreas
APPLICANT: Grairke, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION:
INFORMATION:
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                                                                                                                                                                                                                                               CITY: Sar
STATE: Ca
COUNTRY:
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us-09-981-606-27_copy_6494_6927.rni

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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                      Score 432.4; DB 3; Length 10825; Pred. No. 3.6e-141; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SOURNESS: 44
CORRESPONDENCE ADDRESS:
             LOCATION: replace (3878, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
FEATURE:
NAME/KEY: allele
LOCATION: replace (5834, "g")
OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08652265
Patent No. 6025130
                                                                                                                                                                                                                                                                                      99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTTCTGTTTTAG 434
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
NAME/KEY:
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US-08-652-265-5
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ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

CITY: San Francisco STATE: California

COUNTRY:

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5665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGGCCTTGAACTACCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5726 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCCAATGGGATGGGACCTACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 7107..7147)
LOCATION: double for the following control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION: / Jabel= 24d2
US-08-652-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: -
LOCATION: 140..7319
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
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LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)" REATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265 FILING DATE: 23-MAY-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 432.4; DB 3;
Pred. No. 3.6e-141;
                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 37,23
REFERENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10625 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
99.6%; Score 432.4;
Best Local Similarity 99.8%; Pred. No. 3.6e
Matches 433; Conservative 0; Mismatches
                                                 PC-DOS/MS-DOS
    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
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Best Local Similarity
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241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
                                                                                                                                                                                                                /note= "No. 6140305mal or wild-type (unaffected)
Hereditary Hemochromatosis (HH) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5606 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                                                                                                                   LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: /note= "No. 6140305mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C) OTHER INFORMATION: allele (SEQ ID NO.41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Score 432.4; DB 3; Length 10825; 99.8%; Pred. No. 3.6e-141;
                                                                                                                                                                                                                                                                                                                                                    /note= "start and stop positions for
normal or wild-type (unaffected) allele
cDNA (SEQ_ID NO:9)"
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OTHER INFORMATION: /phenotype= "normal or wild-type OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
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(unaffected) "
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                                                         DNA (genomic)
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NAME/KEY:
LOCATION: 5507..6023
OTHER INFORMATION: no
OTHER INFORMATION: st
OTHER INFORMATION: 8
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Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION: 140.7319
OTHER INFORMATION: //
OTHER INFORMATION: C
FRATURE:
                single
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FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: replace
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NAME/KEY: allele
             STRANDEDNESS:
                                                         MOLECULE TYPE:
                                                                                                   NAME/KEY:
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Matches
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5786 GCTGGATAACCTTGGCTGTACCCCCTGGGGAAGAGCAGAGATATACGTGCCAGGTGGAGC 5845
                                                                                                                                                                           5906 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 5965
                                                                                                                                                                                                                                                                   5966 TGAGGATCTGCTCTTTGTTAGGGGCTGGGCTGGGCTGGCAATCAAAGGCTTTAACTTGC 6025
                                                                                                                                 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA 360
                                                                                                                                                                                                                       TGAGGATCTGCTCTTTGTTAGGGGATGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                                              241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
                                                                                          5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: US 08/652,265
FILING DATE. 23-MAY-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08834497A
Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: WEREDITARY F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIF: 10036-2811
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               TTTTTCTGTTTTAG
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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US-08-834-497A-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5966 TGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 6025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5666 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGACCTACCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: replace (3872, "g")

COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION:

COTHER INFORMATION: /label= 24d2

US-08-834-497A-5
                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 140..7319
OTHER INFORMATION: /note= "start and stop positions for
OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "start and stop positions for
genomic sequence surrounding variant
for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.6%; Score 432.4; DB 3; Best Local Similarity 99.8%; Pred. No. 3.6e-141; Matches 433; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        triricidrificas
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LOCATION: 3852..3891
COTHER INFORMATION: /IOOTHER INFORMATION: GEN
OTHER INFORMATION: FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KBY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-503-444A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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5846 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGAGACTGAGGA 5905
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                                                                                                   301 GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAG 360
                                                                                                                                                                                                                                     361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Preder, John N.
APPLICANT: Reder, John N.
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Ruddhinshi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HERBITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES:
ADDRESSEE: Pennie c pares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 95
SOFTWARE: FeatSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE STRICTURE 314
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION 514
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
CLASSIFICATION: 514
CLASSIFICATION: 514
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-834-497A-5; Sequence 5, Application US/08834497A; Patent No. 6140305
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                   TTTTTCTGTTTTAG 434
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OTHER INFORMATION: allele (SEQ ID NO:41)"
                                                                     NAME/KEY:

LOCATION: 5507..6023

LOCATION: 5507..6023

OTHER INFORMATION: Normel or widoluber in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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Parent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Peder, John N.
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6026 rrrrrcrcrrrrAG 6039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.8°
Matches 433; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-503-444A-1
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Hereditary Hemochromatosis (HH) gene
allele"
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OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: OTHER INFORMATION: OCHER INFORMATION: /note= "No. 6228594mal or wild-type (unaf OTHER INFORMATION: Hereditary Hemochromatosis (HH) gene OTHER INFORMATION: allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3852.3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) genomic OTHER INFORMATION: sequence surrounding variant for 24d2(C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 140.,7319
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: normal or wild-type (unaffected) allele OTHER INFORMATION: CDNA (SEQ ID NO:9)"
                                                                                           APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE:
WordPerfect Version B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
FILING DATE: 13-May-1996
FILING DATE: 13-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
RICH RAPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATOCNEY/AGENT INFORMATION:
NAME: POSISBAIT, BILIN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-95
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: USA
ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
Sequence 1, Application US/09503444A
Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 10825 base pairs TYPE: mucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGGCCTTGAACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAAATGGGGATGGGACCTACCAGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
/note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d1(G) allele (SEQ ID NO:20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                   /phenotype= "normal or wild-type (unaffected)"
/label= 24d2
                                                                                                                                                                                                                                                                                                                                                   /phenotype= "normal or wild-type (unaffected)"
/label= 2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: replace (5834, "g")
OTHER INFORMATION: 'phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Score 432.4; DB 3; 99.8%; Pred. No. 3.6e-141; cive 0; Mismatches 1;
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5606 TGCCTCCTTTGGTGAAGGTGACATCATGTGACCTCTTCAGTGACCACTCTACGGGTGTC 5665
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                                                                                                                                                                                                                                                                                                                                                                                                          61 GGGCCTTGAACTACTACCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA
                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                              Length 10825;
                                          LOCATION: replace (3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
OTHER INFORMATION: /label= 24d2
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Feder, John N. APPLICANT: Feder, John N. APPLICANT: Enuer, Peter M. APPLICANT: Lauer, Peter M. APPLICANT: Lauer, Peter M. APPLICANT: Thomas, Winston APPLICANT: Thomas, Winston APPLICANT: TRUCHINASH, Zenta APPLICANT: Wolff, Roger K. TITLE OF INVENTION: Megabase Transcript Map: No. 587223 TITLE OF INVENTION: Sequences and Antibodies Thereto NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
                                                                                                                                                                                                   99.6%; Score 432.4; DB 3; 99.8%; Pred. No. 3.6e-141; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: TOWNSEND and TOWNSEN: STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                Matches 433; Conservative
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                          NAME/KEY: allele
                                                                                                                                                                                                                              Local Similarity
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ZIP: 94111-3834
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                                                                                                                                                                                                      Query Match
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION:
OTHER INFORMATION: mutation"
OTHER INFORMATION: mutation"
OTHER INFORMATION: gene 24d2 allele"
NAME/KEY:
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OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: 24d2 allele cDNA (SEQ ID NO:11)"
NAME/KEY: .
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LOCATION: 3852.3891

OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"

FRATURE:
NAME/KRY: -
LOCATION: 5507..6023
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genomic sequence surrounding variant
for 24d1(G) allele (SEQ ID NO:20)"
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8907-0088-999
                                                                                                                                                                                                                                                                                                           COUNTY 1 0036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect Version 8
CURRENT APPLICATION DATA:
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
AND AND APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                      SSEE: Pennie & Edmonds LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFRENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                      STREET:
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198329 TTTTTCTGTTTTAG 198342
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not relevant
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARATERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.64;
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Best Local Similarity 99.8
Matches 433; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: not 1
                                                                                                                USA
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                                                                                                                COUNTRY:
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Sequences and Antibodies Thereto
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Pred. No. 2.2e-140;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

// CCATION: 1..246240

// CTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
                                                                                           017957-000100
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Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REPERENCE/POCKET UNMERS: 01795
TELEPHONE: 415-576-020
INFORMATION EN HS-576-0300
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T: Kronmal, Gregory S.
T: Lauer, Peter M.
T: Ruddy, David A.
T: Thomas, Winston
T: Tsuchihashi, Zenta
T: Wolff, Roger K.
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                                                                                                                                                                                               LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8%;
Matches 433; Conservative
 01-OCT-1996
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TITLE OF INVENTION:
FILING DATE:
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US-08-724-394A-21
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197909 TGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 197968
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                                                                                                                                                                                                          CUNTEXT: U.S. S. S. C. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC. Compatible
OPERATING SYSTEM: PC.-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 53 6
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION UNMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
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Pred. No. 2.2e-140;
0; Mismatches 1;
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| COCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21
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198149 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA 198208
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                                                                                                                            198209 GCTGAGAAAICTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
                                                                            GCTGAGAAAATCTATTGGGGGTTGAGAGGAGTGCCTGAGGAGGTAATTATGGCAGTGAGA
                                                                                                                                                                          361 TGAGGATCTGCTCTTTGTTAGGGGATGGGCTGAGGGTGGCAATCAAAGGCTTTAACTTGC
LOCATION: join (361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OCHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION: mutation: OTHER INFORMATION: mutation: OTHER INFORMATION: gene 24d1 allele" (HH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruchinshi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
WIRENT APPLICATION DATA:
APPLICATION NUMBER: 23-MAY-1996
CLASSIFICATION: 514
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Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION UNDRER: 30,23
REFERENCE/DOCKET UNDRER: 17957
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08652265 Patent No. 6025130
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                                                                                                                                                                                                                                                                           TTTTTCTGTTTTAG 434
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LOCATION: 140..7319
OTHER INFORMATION: /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-652-265-3
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                                                                            301
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                                                                                                                                                                                                                                                                                                                           No. 5872237el
                                                                                                                                                                     APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRIES 19411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CIIY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

| LOCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22
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FR: 017957-000100
                                                                  Sequence 22, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179:
TELECOMMUNICATION INFORMATION:
TELERAK: 415-576-0200
INFORMATION FOR SEQ ID NO: 22:
SEQUIENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
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not relevant
E: cDNA
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                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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MOLECULE TYPE:
                                                     JS-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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Best Local
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LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Onote= "start and stop positions for OTHER INFORMATION: CDNA containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles
OTHER INFORMATION: (SEQ ID NO:12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Hereditary Hemochromatosis (Hi
gene containing a combination of both
24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMES/KEY:
LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDRESSEE: Townsend and Townsend and Crew LLI
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265
FILING DATE: 3-MAY-1996
CLIASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 24d2 mutations"
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OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: - 10CATION: 3852..3891
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LOCATION: 140..7319
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OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                            California
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LOCATION:
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                                                                                                                                                                                      LOCATION: 5507..6023
COTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
FEATURE:
NAME/KEY: allele (8334, "a")
COTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis OTHER INFORMATION: /label= 24d1
US-08-652-265-3
                                                   NAME/KEY: -
LOCATION: 3852..3891
LOCATION: Mote= "start and stop positions for OTHER INFORMATION: for penomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
     OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihabhi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
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Best Local Similarity 99.53
Matches 432; Conservative
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APPLICANT:
APPLICANT:
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US-08-652-265-7
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Length 10825;
LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
OTHER INFORMATION:
                                                                                                                                           /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                       Score 430.8;
                                                                                                                                                                                                                                                       99.38;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CILASIFFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POISSAIL, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-9
REFERENCE/DOCKET NUMBER: 8907-0056-9
TELECHANICATION INFORMATION:
TELEPAX: 660-493-556
TELEFAX: 661-493-4935
TELEFAX: 661-4910 NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TEREPAX: 60-493-656
TYPE: NUCLEIC GOLD
STRANDENESS: SINGLE
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NAME/KBY: allele
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NAME/KEY:
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NAME/KEY:
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                                                         1 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC
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                     Gaps
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APPLICANT: Drayra, Dennis T.
APPLICANT: Brayra, Dennis T.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuddy, David
APPLICANT: Tsudhinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
CORRESPONDENCE ADDRESS:
                   Indels
 99.5%; Pred. No. 1.3e-140;
tive 0; Migmatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: NEW 101A
COMPUTER: 10036-2811
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMpatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
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US-08-834-497A-3
; Sequence 3, Application US/08834497A
; Patent No. 6140305
; Patent INFORMATION:
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Best Local Similarity 99.5
Matches 432; Conservative
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5606 TGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACCACTCTACGGTGTC 5665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: replace(5834, "a")

OUTER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                /note= "Hereditary Hemochromatosis (HH)
gene 24d1 allele"
NAME/KEY: CDS
LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..56
LOCATION: 6040..6153, 7107..7147)
OTHER INFORMATION: /product= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 3852..3891
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(C) allele (SEQ ID NO:41)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "start and stop positions for
genomic sequence surrounding variant
for 24d1(A) allele (SEQ ID NO:21)"
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                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "start and stop positions OTHER INFORMATION: 24d1 allele cDNA (SEQ ID NO:10)"
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61 GGGCCTTGAACTACTCCCCCAGAACATCACCATGAAGTGGCTGAAGGATAAGCAGCCAA 120
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                                                                                                          LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, LOCATION: 6040..6133, 7107..7147)
OCHER INFORMATION: /product= "Hereditary Hemochromatosis OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10825,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: replace(3872, "g")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                     and 24d2 mutations" (HH) /note="Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 140..7319
COTHER INFORMATION: /Note= "start and stop positions for OTHER INFORMATION: cDNA containing a combination of both OTHER INFORMATION: 24d1 and 24d2 alleles OTHER INFORMATION: (SEQ ID NO:12)"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -
LOCATION: 3852..3891
LOCATION: JINEORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 5507..6023
OTHER INFORMATION: /note= "start and stop positions for OTHER INFORMATION: genomic sequence surrounding variant OTHER INFORMATION: for 24d1(A) allele (SEQ ID NO:21)"
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99.3%; Score 430.8; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.3e-140;
Matches 432; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= 24d1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: replace (5834, "a")
OTHER INFORMATION: /phenotype
OTHER INFORMATION: /label= 24
                             MOLECULE TYPE: DNA (genomic)
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linear
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                                                                       241 ACCCAGGCCTGGATCAGCCCCTCATTGTGATCTGGGGTATGTGACTGATGAGAGCCAGGA
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Welff, Roger K.
APPLICANT: Welff, Roger K.
APPLICANT: Wolff, Roger K.
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: DATESTED ATTORNEY AGENT AND ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT ATTORNEY AGENT AGENT ATTORNEY AGENT ATTORNEY AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGENT AGEN
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I: 1155 Avenue of the Americas
New York
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEPAONE: 650-493-556
TELERAX: 660-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-834-497A-7
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Search completed: February 11, 2004, 17:12:26 Job time : 56.7163 secs δ₀ qq

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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September 12, 2003, 21:53:18; Search time 109.119 Seconds (without alignments) 6373.435 Million cell updates/sec OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1 atcatgagtgtcgccgt 17 US-09-981-606-30 Scoring table: Perfect score: Sednence: Run on:

5777422 Total number of hits satisfying chosen parameters:

2888711 seqs, 20454813386 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
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GenEmbl:* Database

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15.4 90.6 10.0 0 ARTIS204 15.4 90.6 80.4 9 ARTIS204 15.4 90.6 80.4 9 ARTIS204 15.4 90.6 80.4 9 ARTIS204 15.4 90.6 80.4 9 ARTIS204 15.4 90.6 10.45 9 ARTIS00604 15.4 90.6 10.45 9 ARTIS00604 15.4 90.6 10.73 9 ARZA49337 15.4 90.6 12.80 9 ARZA49337 15.4 90.6 13.70 6 ARXA07339 15.4 90.6 13.70 6 ARXA07339 15.4 90.6 14.40 6 ARI17794 15.4 90.6 14.40 6 ARI17794 15.4 90.6 14.40 6 ARI149463 15.4 90.6 15.5 6 ARI19203 15.4 90.6 15.5 6 ARI19203 15.4 90.6 15.5 6 ARX00319 15.4 90.6 15.5 6 ARX00319 15.4 90.6 27.27 9 ARX00319 15.4 90.6 27.27 9 ARX00319 15.4 90.6 93.42 1 BPETOXOP 15.4 90.6 93.42 1 BRETOXOP 15.4 90.6 93.42 93.44 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 15.4 90.6 93.42 93.44 90.6 93.45 93.44 90.6 93.45 93.44	Η,			9/		AXUBUL84	
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AR199266	Sequence AR199266	AR19926		Unknown.	Unknown.	Unclassified.	1 (bases 1 to 17)	Rothenb	Mutatio	Patent:	
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Unclassified.
1 (bases 1 to 32)
Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.
Hereditary hemochromatosis gene products
Patent: US 6440305-A 44 31-OCT-2000;
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1 (bases 1 to 17)
Rothenberg, B.E., Sawada-Hiral, R. and Barton, J.C. Mutations associated with iron disorders
Patent: US 6509442-A 30 21-JAN-2003;
Location/Qualifiers
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PAT 18-MAR-2002
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PAT 08-AUG-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
Patent: US 6228594-A 44 08-MAY-2001;
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/organism="Homo sapiens"
/moi_type="genomic DNA"
/db_xref="taxon:9606"
/note="Defection de la mutation H63D dans le gene de
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/note="Defection de la mutation H63D dans le gene de
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100.0%; Pred. No. 1.3e+02;
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Sequence 43 from Patent W00214555.
AX393579
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Sequence 11 from Patent W00212557.
     32 bp
Sequence 44 from patent US 6228594.
ARI49496
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PAT 08-AUG-2001
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1 (bases 1 to 40)

Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
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Hereditary hemochromatosis gene products
Patent: US 6140305-A 41 31.0CT-2000;
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Sequence 41 from patent US 6228594.
AR149493
AR149493.1 GI:15114084
Patent: US 6228594-A 43 08-MAY-2001;
Location/Qualifiers
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Best Local Similarity 94.1%;
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                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
                                                                              Wittwer, C.T., Crockett, A.O., Caplin, B.E., Stevenson, W., Wagner, L.A., Chen, J. and Kusukawa, N. Single-labeled oligonucleotide Pubes Single-labeled oligonucleotide Pubes Patent: WO 0214555-A 43 21-FEB-2002; University of Utah Research Foundation (US); Idaho Technology,
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Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
Hereditary hemochromatosis gene products
Patent: US 6140305-A 43 31-0CT-2000;
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Sequence 43 from patent US 6140305.
AR117825
AR117825.1 GI:14098731
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AR149495
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PAT 22-FEB-2001
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Sequence determination of nucleic acids using electronic detection
Patent: WO 0107665-A 37 01-FEB-2001;
Clinical Micro Sensors, Inc. (US)
Location/Qualifiers
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AX080199 75 bp
Sequence 37 from Patent W00107665.
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Sequence 22 from Patent WO0107665.
AX080184
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Patent: WO 02070755-A 207 12-SEP-2002;
Third Wave Technologies, Inc. (US)
Location/Qualifiers
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PAT 22-FEB-2001

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Methods for generating databases and databases for identifying polymorphic generic markers
Patent: WO 0127857-A 110 19-APR-2001;
Sequenom, Inc. (US)
Location/Qualifiers
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/organism="Homo sapiens"
//mol_type="genomic DNA"
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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SUMMAKIES			ID		AAA96797	AAC68462	ABL56391	AAK98989	AAC68461	AAC68459	AAH78015	AAF58246	
			DB		21	22	24	24	22	22	22	22	
			Length	,	17	32	30	31	32	40	47	7.5	
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	15	S	90.6	1440	22	AAC68430	Human hereditary h
	16	2	90.6	2506	21	AAA96769	CDNA sequence enco
	17	S	9.06	2727	19	AAV23525	Haemochromatosis o
	18	S	9.06	5982	25	ABV93934	Human colon specif
ບ	13	S	9.06	7742	18	AAT84745	Bordetella pertuss
	20	S	9.06	10825	18	AAT96690	Hereditary haemoch
	21	S	9.06	10825	22	AAC68425	Human hereditary h
	22	15.4	90.6	10825	22	AAC68426	
	23	'n.	90.6		21	AAA96794	Genomic DNA of a h
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O	25	٠ دم	90.6		19	AAV57903	Hereditary haemoch
	26	4	84.7	20	22	AAH55966	
O	27	4	84.7	234	25	ABZ41768	N. gonorrhoeae nuc
Ö	28	4	84.7	370	22	AAH55800	Human SCN2A genomi
	29	14.4	84.7	734	21	AAA82008	N. meningitidis pa
Ö	30	4	84.7	1791	24	ABK73785	Bacillus lichenifo
	31	4	84.7	1920	23	ABL08807	
O	32	4	84.7	4134	23	ABL08808	Drosophila melanog
U	33		84.7		23	ABL08806	Drosophila melanog
O	34	4	84.7	49980	21	AAF21607	Neisseria meningit
O	35	4.	84.7	1437668	21	AAA814 90	N. meningitidis B
Ö	36	14	82.4	65	24	ABN29608	Rat spliced transc
O	37	14	82.4	375	24	ABK79755	Bacillus clausii g
U	38	14	82.4		23	ABL03186	Drosophila melanoq
O	39	-	82.4	129021	21	AAF22296	BAC containing rep
O	40	ω.	81.2	27	24	AAK98987	Human probe HHDP2
ပ	4,1	m m	81.2	27	4	AAK98988	Human probe HHDP3
O	42	ω,	81.2	28	4	AAK98986	HHDP
	43	13.8	81.2	30	24	ABL56392	ed qene fra
	44	-	81.2	31	4	AAK98990	Human probe target
	45	m	81.2	40	(7	AAC68460	ace surroun
						0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
						ALLGNMENTS	
RES	RESULT 1						
AAA	AAA96797						
A ;	AAA9	AAA96797 st	standard; DNA;		17 BP	·	

Probe for detecting histocompatibility iron loading gene mutation 865C. Human; histocompatibility iron loading protein; HFE protein; major histocompatibility complex; non-classical class I gene; chromosome 6p; iron disorder; haemochromatosis; probe; ss. Barton JC; Sawada-Hirai R, (BILL-) BILLUPS-ROTHENBERG INC. 24-MAR-2000; 2000WO-US07982. 99US-0277457 (first entry) WO200058515-A1. Rothenberg BE, Homo sapiens. 26-MAR-1999; 19-FEB-2001 05-OCT-2000.

AAA96797;

Diagnosing an iron disorder e.g. hemochromatosis or a genetic

WPI; 2000-647244/62

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Query Match
                             AAC68462;
                                                 Feder JN;
                          RESULT 2
                          AAC68462
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The present sequence represents a probe which is used to detect the mutation S55C in the human histocompatibility iron loading (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-classical class I gene located on chromosome 6p. Mutations in the gene lead to iron disorders. The specification describes a method for diagnosing an iron disorder or a genetic susceptibility to develop the disorder in a mammal. The method comprises determining the presence of a mutation in exon 2 or an intron of a HFE gene or protein. The mutation is not a C for 6 missense mutation at nucleotide 187 of the sequence given in A96769 (Genbank Accession number 160319). The presence of the mutation indicates the disorder or the genetic susceptibility to the disorder. The method is used to diagnose an iron disorder e.g. haemochromatosis, or a genetic susceptibility to develop it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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susceptibility to develop it, by determining the presence of a mutation in exon 2 or an intron of a histocompatibility iron loading nucleic acid -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 17; DB 21; 100.0%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hereditary hemochromatosis gene products for treating hereditary hemochromatosis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruddy D,
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                                                                                                                               Example 1; Page 29; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drayna DT, Gnirke A,
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Matches 17; Conservative
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as

The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed a having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for

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The present sequence represents a fragment of the gene to which probe ABL539 hybridises. This probe was used to detect the mutation H63D, which is responsible for hemochromatosis. The probe is used to demonstrate the method of the invention. The specification describes a method for detecting a mutation at position in a target nucleic acid by solid phase amplification process. The region of interest is amplified on at least two separate supports (A, B) using at least one primer linked, at its 5'-end, to the supports. The DNA strands are then separated and strands in the suspension removed by washing. Bound DNA sequences are hybridized to a probe, the 3'-end of which hybridizes up to, at most, position n-1. The probe is elongated by BOLYMERTS and an uncleotides in the 5' to 3' direction, using a DNA polymerase and a nucleotides in the 5' to 3' direction, using a DNA polymerase and a nucleotide derivative (durr*) that is resistant to exonuclease. The dNTP* used is complementary to the mutation for support A but to the wild type for supports are not degraded by dNTP* are not degraded. The supports are then washed and non-degraded probes detected inflictily. The method is used to detect mutations associated with an exonuclease, especially haemochromatosis; sickle-cell anaemia; alpha or beta-thalassemia; cystic fibrosis; haemophilia; neurodegeneration and entire mentific region and for detering and/or identifying gene or an entire mentific region and for detering and/or identifying appears and an entire mentifically
alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutation; solid phase amplification; haemochromatosis; cancer; sickle-cell anaemia; beta-thalassemia; alpha-thalassemia; polymorphism; cystic fibrosis; haemophilia; neurodegeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entire genetic region and for detecting and/or identifying genetically modified organisms.
                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting mutations in nucleic acid, useful e.g. for diagnosing haemochromatosis, by solid phase amplification to incorporate exonuclease resistant nucleotide
                                                                                                      Length 32;
                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene fragment which when mutated causes haemochromatosis.
                                                                                                      DB 22;
                                                            BP; 5 A; 5 C; 11 G; 11 T; 0 other;
                                                                                                                         6.4;
                                                                                                                                               Mismatches
                                                                                                      Score 17;
Pred. No.
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                                                                                                                                               0,
                                                                                                      100.0%;
                                                                                                                                                                                    1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                            10 ATCATGAGIGICGCCGT 26
                                                                                                                                                                                                                                                                                                                               ABL56391 standard; DNA; 30 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                       Best Local Similarity 100.
Matches 17; Conservative
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                                                            Sequence 32
                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cailloux F,
                                                                                                                                                                                                                                                                                                                                                                         ABL56391:
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                          RESULT 3
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Homo sapiens.
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23-MAY-1996;
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                                                                                                                                       21-FEB-2001
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                                                                                          AAC68461:
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         RESULT 5
                               AAC68461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new probe for analysing a target nucleic acid comprising of a fluorescent detecting entity consisting of a single-labelled oligonucleotide having a sequence complementary to a locus of the target nucleic acid and a fluorescent label linked to an internal residue of the oligonucleotide. The probe is useful in melting curve analysis, agencypting, detecting pathogens such as Salmonella, and in biological sample. This polynucleotide sequence represence in a biological sample. This polynucleotide sequence represents a probe target of the invention for melting analysis of haemochromatosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human probe target HHDT1 of haemochromatosis-associated mutation C187G.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New probe useful for e.g. genotyping, comprises a single-labelled oligonucleotide having a sequence complementary to a locus of the target nucleic acid and a fluorescent label linked to an internal residue of the oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fluorescent detecting entity; melting curve analysis; genotyping; pathogen; probe; human; Factor V Leiden mutation; target; ss.
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                                                                 Length 30;
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                                                                                                            Indels
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                                                               DB 24;
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                    Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 other;
                                                          Score 15.4; DB
Pred. No. 51;
0; Mismatches
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                                                                                                          0
                                                               90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2001; 2001WO-US25231.
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2000US-240610P.
                                                                                                                                                1 ATCATGAGTGTCGCCGT
                                                                                                                                                                         5 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                   AAK98989 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                          Conservative
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Best Local Similarity
16; Conserve
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                                                                                 Similarity
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                                                        Query Match
Best Local Simi.
Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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16-OCT-2000;
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having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                  HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%; Score 15.4; DB 22;
94.1%; Pred. No. 51;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HH; hereditary hemochromatosis; chelation agent; T-cell differentiation factor; iron overload; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32 BP; 6 A; 5 C; 11 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruddy D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence surrounding HH mutation 24d2 c.
                                                                                                                           Sequence surrounding HH mutation 24d7a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 21; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gnirke A,
AAC68461 standard; DNA; 32 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                            96US-0630912.
96US-0632673.
96US-0652265.
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                                                                                                                                                                                                                                                                                                                                                     97US-0834497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC68459 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas WJ, Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006341/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 16; Conserv
                                                                                                                                                                HH; hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6140305-A.
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0;

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Gaps

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Indels

1;

Pred. No. 51;

δ qq

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The specification describes a method for detecting a mutation at a particular position in a target nucleic acid. The method comprises binding the target to a solid support, hybridizing a probe to the target, elongating the probe with howelecchide(s) resistant to exonuclease, digesting the probe with exonuclease and detecting bound nucleic acid. The mutation is in position "" in a target nucleic acid and the 3' extremity of the probe hybridises to position "". The method is used to detect gene mutations implicated in disease, particularly hereditary genetic diseases, especially sickle cell anneals, alpha and beta thalassemias, cystic fibrosis, hemophilia and genes implicated in cancer. The present sequence represents a DNA fragment which comprises a mutation which is implicated in hemochematosis. The mutation is detected using the method of the
       Detecting mutation in target nucleic acid, useful for detecting hereditary genetic diseases, comprises using chip whose electrical or optical property changes relative to the presence of hybridized probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47 BP; 7 A; 12 C; 15 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; DB
Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                       French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%;
ilarity 94.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999; 99US-0145695, 17-MAR-2000; 2000US-0190259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCATGAGIGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF58246 standard; DNA; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                   Example 4; Page 17; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide D1121
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
16; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-159728/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200107665-A2.
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                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF58246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Umek RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58246,
           δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA mutation; hereditary genetic disease; sickle cell anemia;
thalassemia; cystic fibrosis; haemophilia; cancer; haemochromatosis; ds.
                                                                                                                                                                                         Wolff RK;
                                                                                                                                                                                                                                                                         New hereditary hemochromatosis gene products or polypeptides, useful for treating hereditary hemochromatosis in a patient, and as a metal chelation agent alleviating iron overload -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a mutation which is implicated in haemochromatosis.
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                                                                                                                                                                                       Tsuchihashi Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 40;
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"this base is mutated to G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.6%; Score 15.4; DB 22;
94.1%; Pred. No. 52;
Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40 BP; 7 A; 7 C; 13 G; 13 T; 0 other;
                                                                                                                                                                                         Ruddy D,
                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 20; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                    Gnirke A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                           96US-0632673.
96US-0652265.
                                    97US-0834497
                                                                         96US-0630912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH78015 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                             (BIRA ) BIO-RAD LAB INC.
                                                                                                                                                                                    Drayna DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
/note=
                                                                                                                                                                                                                                        WPI; 2001-006341/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA mutation;
                                    04-APR-1997;
                                                                         04-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA fragment
                                                                                           16-APR-1996;
23-MAY-1996;
31-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                  Thomas WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001
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RESULT 7 AAH78015 AAH78015;

Query Match

Best Loc Matches

δŽ a Key mutation

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Gaps

Matches

a δλ

2 **x** 8

us-09-981-606-30.rng

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The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
                                                                                                            polymorphism; SNP; human; genetic marker; djsease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiincer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 100;
                                                              Human HLA-H exon 2 coding sequence fragment SEQ ID NO: 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 100 BP; 19 A; 22 C; 29 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ping Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and entering the information into a database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.4; DE
Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Boom D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 303; 304pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
0
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                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0217251.
2000US-0217658.
2000US-0663968.
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94.18;
                                                                                                                                                                                                                                                                                                                                               13-OCT-2000; 2000WO-US28413
                                                                                                                                                                                                                                                                                                                                                                                                        99US-0159176
             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koester H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-273865/28.
                                                                                                                                          drug response; ds
                                                                                                                                                                                                                                           WC200127857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2000; 2
10-JUL-2000; 2
19-SEP-2000; 3
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             12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1999;
                                                                                                                                                                                                                                                                                              19~APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jurinke C;
                                                                                                              Database;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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          NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                          0;
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                                                                                                      Length 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                Sequence 75 BP; 21 A; 24 C; 16 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 76 BP; 21 A; 24 C; 17 G; 14 T; 0 other;
                                                                                                 Score 15.4;
Pred. No. 56;
                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; |
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CLIN-) CLINICAL MICRO SENSORS INC
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                                                                                                 90.6%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
94.1%;
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2000US-0190259,
monitoring gene expression.
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ID AAF58231 standard; DNA; 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-159728/16.
                                                                                                                         Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single surface
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                                                                                                                                               16;
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                                                                                                 Query Match
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Ruben SM;
29-SEP-2000; 2000US-023656.
29-SEP-2000; 2000US-023656.
29-SEP-2000; 2000US-023656.
29-SEP-2000; 2000US-023656.
29-SEP-2000; 2000US-0236570.
02-OCT-2000; 2000US-0236870.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237039.
02-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-0241787.
20-OCT-2000; 2000US-0246677.
08-NOV-2000; 2000US-0246521.
17-NOV-2000; 2000US-0246521.
17-NOV-2000; 2000US-0246521.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-024921.
17-NOV-2000
 2000US-0236367.
2000US-0236368.
2000US-0236379.
2000US-0236379.
2000US-0236379.
2000US-0236379.
2000US-0237038.
2000US-0237039.
2000US-0237040.
2000US-0237040.
2000US-0237040.
2000US-0237040.
2000US-0237040.
2000US-024186.
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      2000US-0179065.
2000US-0186628.
2000US-01866364.
2000US-0189874.
2000US-0189874.
2000US-0189874.
2000US-0189875.
2000US-0189876.
2000US-018987.
2000US-0189876.
2000US-018988.
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2000US-0235836.
2000US-0236327.
                                          17-JAN-2001; 2001WO-US01309
                                                                       31-JAN-2000;
04-FEB-2000;
02-FEB-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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              02-AUG-2001
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Laham N;

Rotem-Yehudar R,

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Soluble beta 2 microglobulin/HFE monochain useful for treating iron-overload conditions e.g. thalassemia and chronic infections, comprises human beta 2 microglobulin linked to alpha domains of HFE by
                                            WPI; 2002-383192/41.
                                                                                                                              a linker peptide
                                                         P-PSDB; AAU80035
                Ehrlich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT96691
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                                                                                                                 The Invention relates to immune, porty, western the concided proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemias, (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                           The invention relates to human polynucleotides (AAI63803-AAI64012) and
                                                                                                                                                                                                                                                                           (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasittic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iron absorption regulator; intracellular iron absorption; lung injury; haemochromatosis; transfusion; thalassaemia; haemolytic anaemia; chronic infection; transferrin receptor; TfR; brain tumour; cancer; oxidative stress disorder; tissue damage; vascular disease; inflammation; atherosclerosis; autoimmune disease; inflammatory condition; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                       New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 596;
                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 596 BP; 133 A; 157 C; 175 G; 126 T; 5 other;
                                                                                  664pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; I
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 94.1
Matches 16; Conservative
                                                                                SEQ ID NO 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..1317
/*tag=
WPI; 2001-488781/53
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              P-PSDB; AAM43591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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thalassaemias, haemolytic anaemia or chronic infections, and for delivering a therapeutic to cells that over-express transferrin receptor (TfR) which are preferably lymphocytes or leukocytes, across the bloodbrah brain bearier. (I) is further useful for treating brain tumour. (I) is also useful for treating oxidative stress disorders resulting in tissue of tissue damage e.g. vascular diseases, inflammation, atherosclerosis, under injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful as a platform for drug delivery of therapeutic use for cancer, arother decases and inflammatory conditions. The monochain manifests specific characteristics advantageous for drug delivery systems. It is a soluble, stable and fully conformed protein. It binds specifically to transferrin receptor (TfR) and therefore targets cells that over-express this receptor. It is continuously internalised by the target cells, thus enabling efficient drug delivery. It dissociates from the receptor in the cells, in inimising side effects. It negatively regulates iron absorption, reducing growth of undesired cells and preventing lymphocyte activation.

It is not diluted in the blood as is transferrin. It should not induce an immune response since it is a self non-polymentic protein and delivery of annochain is a self non-polymentic protein and delivery of annochain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                       The invention relates to a soluble polypeptide (1) of beta 2 microglobulin (beta2m)/HFE monochain comprising human beta2m (or its analogue or active fragment), linked to alphal-alpha3 domains of human HFE (a central regulator of iron absorption; undefined), or its analogue or active fragment, by a flexible linker peptide, or a functional derivative or salt of (1). (1) is useful for reducing intracellular iron absorption in patients having hereditary hammochromatosis, transfusions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drugs via monochain is expected to overcome drug-resistance since it is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%; Score 15.4; D
94.1%; Pred. No. 79;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coding sequence of beta2m/HFE monochain.
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222.1268
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Example 2; Fig 2; 77pp; English.
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This cDNA clone, designated cDNA24, is derived from human gene whose mutated form is associated with hereditary haemochromatosis (HH). It was obtained from a directionally cloned plasmid-based CDNA library following identification of the HH locus in the HLA region of chromosome 6. A single mutation (24d1) in the HH gene appears responsible for the majority of HH disease. This comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. It results in a chromosomes and in 4% of unaffected chromosomes. It results in a critical disulphide bridge important for secondary structure. The critical disulphide bridge important for secondary structure. The AAP96690, the H437 bp CDNA sequence (Ia) and thair 24d1, 24d2 and 24d7, variants; a clonding or expression vector; host cells; a peptide product chosen from the HH gene product, its variants (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid residues of these; an antibody produced using the peptide; a method conducts, T-cell differentiation factors and therapeutic agents for mutation; an annial madel for the HH disease; metal of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process in vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process on vivo or mitigation of injury due to oxidative process or product of a nucleic acid sequence as above; and oligonucleotide directed against a transcriptional product of a nucleic acid sequence as above; and oligonucleotide sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence of a nucleic acid sequence for the HH ho
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                                                                                                                                                           "G to A substitution (24d1 mutation
associated with HH), results in Cys to
Tyr substitution"
"C to G substitution (24d2 mutation) results in His to Asp substitution"
                                                                                "A to T substitution (24d7 variant) results in Ser to Cys substitution
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Tsuchihashi Z, Wolff RK;
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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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Pred. No. 79;
                                                                                                                                                                            Human hereditary hemochromatosis cDNA
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Length 1440;

Score 15.4; DB 18; Pred. No. 79;

90.68; 94.18;

Query Match 90.6 Best Local Similarity 94.1 Matches 16; Conservative

Homo sapiens.

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The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B. (bases 1 to 908)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://inage.llnl.gov
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ORGANISM
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TITLE
JOURNAL
COMMENT
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BG506985 601861617
CC075265 CSU-K33r
BY352115 BY352115
                                                                                                                                  (without alignments)
3975.400 Million cell updates/sec
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                                                                                                                  September 12, 2003, 23:31:00; Search time 103.933 Seconds
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                                                                                                                                                                                                                                                                                                                                     45562784
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
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score greater than or equal to
and is derived by analysis of
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gb_gssl:*
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17
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DB

Minimum | Maximum |

Database

Result Š

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Searched:

Sequence:

Title: Perfect :

us-09-981-606-30.rst

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BY352115 RIKEN full-length enriched, whole joints Mus musculus CDNA clone LB30026007 5', mRNA sequence.
BY352115 GI:26581603
                                                                                                                                                                                                                                                                                                                                                        CCU/5265
CSU-K33r.7G6.SP6 CSU-K33r Aedes aegypti genomic clone CSU-K33r.7G6, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-3543
Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.
Seq primer: SP6
Class: BAC ends.
    by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

1.42 c. 127 g. 165 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Bukaryota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
End sequencing of Aedes aegypti BACs
Unpublished
Other_GSSs: CSU-K33r,766.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                    Gaps
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0
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94.1%; Pred. No. 6.5e+02;
Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Rexville"
/db_xxef="texxon:1159"
/clone="CSU-K331.766"
/clone="Lb="CSU-K331"
/note="Vector: pBeloBAC11; Site_1: HindIII"
47 c 65 g 62 t
                                                                                                                                        Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                   Score 16; DB 10; Length 68
Pred. No. 4.7e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .270
                                                                                                                     94.1%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CC075265
CC075265.1 GI:29916787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan Loftus
                                                                                                                                                                                                                                                                    631 ICATGAGTGTCGCCGT 616
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                                                                                                                              Query Match
Best Local Similarity 100.
Matches 16; Conservative
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ORIGIN
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ORGANISM
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JOURNAL
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VERSION
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KEYWORDS
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CC075265
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BY352115
LOCUS
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                                                                                                                                                                 /done_lib="MingMgC_121"
//done_lib="WingMgC_121"
//done_lib="NingMgC_121"
//done_"Organ: brain, Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: ECORV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (ECORV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3:5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dlone="IMAGE:101077"
/lab_host="DH10B (Il phage-resistant)"
/lab_host="DH10B (Il phage-resistant)"
/lone="long" Wac_77"
/hote="Organ: lung; Vector: pDRR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGAGGTGT(30)BN-3' (where B = A,
c, or G and N = A, C, G, Or T). Average insert size 1.9
kb (range 0.5-4.0 kb): 12/15 colonies contained inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG506985 684 bp mRNA linear EST 27-MAR-2001 601861617F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4071077 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I thases 1 to 684)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs_remail.nih.gov
Tissue Procurement: CLOWTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Preparation: CLOWTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM916 row: b column: 06
High quality sequence stop: 469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 17; DB 12; 100.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
High quality sequence stop: 708.
Location/Qualifiers
                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:5240735"
                                                                                                                                                      /lab_host="DH10B"
                                                                                       /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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BG506985.1 GI:13468502
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Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM

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CEE (bases 1 to 344)

Rasudaki,Y., Furuno,M., Rasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
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A.S., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Saptou,M.,
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Karanabe,Y., Walla,S., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
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Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishiia
Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
K.S., Rogers,J., Birney,E., and Hayashizahi, W., Sasaki,D., Shibata
K.S., Rogers,J., Birney,E., and Hayashizahi, W. Battional annotation
of Go,770 full-length conse transcriptome based on functional annotation
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 344)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                     /tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
97 c 96 g 77 t
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iive 0; Mismatches 1;
                                                    /organism="Mus musculus"
                                                                                     /mol_type="mRNA"
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
KIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Labbratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figure 1 genome-resease.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Aizawa,K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishia,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,

Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,

Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami

M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct

Submission
                                                                                                                                                                                                                         Kiyosawa, H.
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                          Bono, H., Kondo, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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                                                                                                                      (bases 1 to 325)
(Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kond Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyo Yaqi,K., Tomatu,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
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Mus musculus
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MEDLINE PUBMED

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FEATURES

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Length 325; Indels

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P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pertovsky, N., Pillai, R., Pontlus, J.U., Qi.D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taylor, M.S., Tasadale, R.D., Tomita, M., Varado, R., Wagner, L., Wahlestedt, C., Rangisawa, M., Yang, L., Yang, E.C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Kang, Y., Carninci, P., Hayatsu, N., Hirozane Rishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizome, W., Imoreni, K., Shihi, Y., Itob, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, Analysis of the mouse transcriptome based on functional annotation of 60,770 full length cobas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resegsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Alizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
"T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
"M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 8145-503-922
Fax: 81-45-503-9216
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Please visit our web site (http://genome.gsc.riken.go.jp)
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Pred. No. 7.3e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/strain="C57BL/6J"
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 346)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H. Yagi,K., Tomaru,Y., Basqawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schrimi,L.M., Kanapin,A., Marsuda,H., Batalov,S., L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Goldy,J., Grimmond,S., Garstincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanal,A., Kawaja,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
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                                            Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY210730

346 bp mRNA linear EST 10-DEC-2002
BY210730 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
cells Mus musculus CDNA clone F730317N09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                      Konno, H., Miyazaki, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11
+ve dendritic cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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              T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J.,
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Pred. No. 7.2e+02;
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/clone="F730024B08"
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94.18;
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Nikaidol; Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Haseqawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Batalov, S., Baisel, K.W., Blake, J.A., Bradi, D., Bursic, V., Chothia, C., Corbani, L.E., Cousins, S., Gaasterland, T., Garibold, M., Gissi, C., Godzik, A., Gody, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Gogoph, J., Kanai, A., Kurochkin, T.V., Lee, Y., Lenhard, B. L., Konagaya, A., Kurochkin, T.V., Lee, Y., Lenhard, B. L., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, F.A., Maglott, D. Ramachandran, S., Ravasi, T., Red, J. U., Oi, D., Ramachandran, S., Ravasi, T., Red, J. U., Oi, D., Ramachandran, S., Ravasi, T., Red, J. U., Oi, D., Ramachandran, S., Ravasi, T., Red, J. U., Oi, D., Ramachandran, S., Ravasi, T., Red, J. U., Oi, D., A., K.D., Tomita, M., Sahmada, K., Sultana, R., Taylor, M.S., Teasdale, R.D., Tomita, M., Sakazume, N., Hachestedt, C., Wangisawa, M., Sakazume, N., Hirozane-Kishikawa, T., Konno, H., Nakawu, R., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imagawa, A., Hashizume, W., Imagawa, R., Sakazume, N., Sa
                                                                                                                                                                                                                                                                                                                          BY327323 RIKEN full-length enriched, synovial fibroblasts Musmusculus cDNA clone L030041G21 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishli,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare full-length count libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE PUBMED

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maus muslais Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basaki,Y. Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomanu,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Balake,J.A., Bradt,D., Brusis,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., Jarvis,B.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Majott,D.R., Mattais,L., Marchin,I.V., Pertea,G., Petrovsky,N., Pillai,R., Pontius,J.G., Qi,D., Ranachanaran,S., Ravasi,T., Reed,J.C., Reed,J.J., Reid,J., Rayana,R., Sullana,R., Sulmana,R., Sullana,R., Jakenaka,Y., Takanabe,Y., Wells,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L., Yang,L., Kang,L., Kawai,J., Alakawa,T., Konno,H., Nakamura,M., Saraume,M., Saraume,M., Saraume,M., Saraume,M., Saraume,M., Saraume,M., Saraumish,M., Kagawa,T., Moshibata,K., Yang,L., Yashinada,X., Haraza,A., Hashizume,M., Waterston,R., Tich,M., Kagawa,T., Miyazaki,A., Yashinada,X., Tander
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                        prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, synovial
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Pred. No. 7.3e+02;
0; Mismatches 1; Indels 0)
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94.18;
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Best Local Similarity 94.1
Matches 16; Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1017-1030 (2000)

RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

DIVISION OF EXPERIMENTAL ALIMENTAL RESEARCH IN RIKEN.
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BY206107.1 GI:26385983
                                                                                                                                                                                                                                                                                                                                               Email: genome-rosigsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
A.T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission
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                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(68C), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Sughiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236 0004 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. and Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length charseriptome based on functional Nature 420, 563-573 (2002)
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1larity 94.1%; Pred. No. 7.3e+02;
Conservative 0; Mismatches 1;
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/mol_type="mRNA"
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                                                                                                                                                                  Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                          Submission
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LOCUS
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Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1el: 81-45-503-922
Fax: 81-45-503-9216
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                            /clone="F730222A16"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RYKEN full-length enriched, B6-derived CD11
+ve dendritic cells"
106 c 104 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY170353 RIKEN full-length enriched, bone marrow macrophage Musmusculus cDNA clone I830082A04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                              Length 357;
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                                                                                                                                                                                                                                                                                                                               Score 15.4; DB 13;
Pred. No. 7.4e+02;
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1. .357
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/63"
                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                    90.6%;
94.1%;
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Best Local Similarity
Matches 16; Conserv
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prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research forup in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse trisques.
URL:http://genome.gsc.riken.go.jb/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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BY202250 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730112A15 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 364)
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further details.
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                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse CDNAs Compared W
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs
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/clone_lib="RIKEN full-length enriched, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissues were provided by David A. Hume ( Depts. of Biochem and Microbiology/Parasitology institute for Molecular Biosc University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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/tissue_type="bone marrow"
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1. .359
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Length 364;

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286 ATCAIGAGAGICGCCGI 302
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                                90.6%;
94.1%;
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Ouery Match
Best Local Similarity 94...
Local 16; Conservative
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AUTHORS
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                                                   veuguin., valumouuu, s., vaustuncicuis., hiroxawa, N., Jackson, J.J.,
Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,
King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Leehard, B., Lyons
P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki
H., Nagashima, T., Numata, K., Okido, T., Perta, G.,
Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring
Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring
B.Z., Ringwal, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale
M., Shimada, K., Sultana, R., Wapner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Walls, C., Wilming, L.G., Wynnaw-Boris, A., Yanagisawa
M., Sakazume, M., Kang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii
Y., Itoh, M., Kagwa, I., Miyazaki, A., Sakai, K., Sakai, D., Shibata
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander
E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence full-length cDNA encyclopedia: real-time sequence full-length cDNA incorration of a nonredundant cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,M., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                        Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
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/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, B6-derived CD11
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-45-503-9222
Fax: 81-45-503-9216
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MEDLINE PUBMED JOURNAL

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Mammalia, Eutralia; Rodentia; Sciulogiacin; Mulidac; Nogami, A., Schonbach, C., Yagir, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagir, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Hume, D.A., Quackenbush, J., Schrill, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bult, C., Hume, D.A., Corban; J. E., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.B., Multais, L., Marchionni, L., McKenzie, L., Mil, Mil, M., Sacholi, C., Pertca, G., Pertca, G., Pertca, G., Pertca, G., Pertca, S., Canadelin, A., Schneider, C., Semple, C.A., Setou, R., Shimada, K., Sultana, R., Pontius, J.U., Reid, J., Rang, I., Kang, I., Wann, Y., Taylor, M.S., Tasadale, R.D., Tang, I., Wann, Y., Werardo, R., Wapner, L., Wahiestedt, C., Wann, Y., Man, Y., Yangi, Sawa, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, Y., Itoh, M., Sakazume, N., Kagwa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, Y., Loth, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, Y., Loth, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Shibata, Y., Yangisis of the mouse transcriptome based on functional annotation of 60, 700 full-length conservation of functional annotation of 60, 700 full-length conservation of functional annotation of 60, 700 full-length conservation of functional annotation of 60, 700 full-length conservation of full conservations of full conservations of full conservations of full conservations of full conservations of full conservations of ful
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Inctani,K., Ishi,Y., Itch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Taqami,M., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
From Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Normalization and subtraction of cap-trapper-selected cDNAs to
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                                                                                                           Gaps
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Score 15.4; DB 13;
Pred. No. 7.4e+02;
                                                                                                           0; Mismatches
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                   sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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RIKEN integrated sequence analysis (RISA) system--384-format
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/tissue_type="bone marrow"
/cell_type="macrophage"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fonno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please wisit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Tackitute of Physical and Chemical Research (RIKEN)
Tel: 22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of captrapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length CDNA
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/clone_lib="RIKEN full-length enriched, B6-derived CD11
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94.1%; Pred. No. 7.6e+02;
ive 0; Mismatches 1;
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                              Nature 420, 563-573 (2002)
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Matches 16; Conservative
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CREAKLY, Y. FURINDO, W. KASUKAWA, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagal, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Osato, N., Salto, R., Bult, C., Hune, D.B., Ouckenbush, J., Schriml, L.M., Ranapin, A., Bult, C., Hune, D.B., Ouckenbush, J., Schriml, L.M., Ranapin, A., Matsuda, H., Batach, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Godyh, J., Grimmond, T., Gariboldi, M., Gissi, C., Godzik, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehrard, B., Lyons, P.A., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Perrovsky, N., Pillai, R., Portius, J.U., Oi, D., Lyons, P.A., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Perrovsky, N., Pillai, R., Pontius, J.U., Reid, J., Reid, J., Ring, R.D., Tomita, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sulmaina, P., Wanshaw-Boris, A., Yanagiz, Yan
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Normalization and subtraction of Cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://genome-gsc.riken.go.jp,
Aizawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S., Hirozane
Aizawa.K., Akimura,T., Arakawa.T., Kono,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Kono,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
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PUBMED
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                  REFERENCE
                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0209"
/note="Corgan: lung-tumor; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 7716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY313216 RIKEN full-length enriched, osteoclast-like cell Musmusculus CDNA clone 1420003G14 5', mRNA sequence.
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 384)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=PM4&t2=PM4-ET0209-151200-003-f07&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 384.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
               PM4-ET0209-151200-003-f07 ET0209 Homo sapiens CDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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87 q 93 t
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                                                                               BF883952.1 GI:12274078
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                                                                                                                                                       Homo sapiens (human)
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Matches 16; Conservative
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               DEFINITION
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SOURCE
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Surgery

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Patent No. 6509442

JERURAL INFORMATION:
APPLICANT: Rothenberg, Barry E.
APPLICANT: Sawada-Hiral, Ritsuko
APPLICANT: Barton. James C.
TITLE OF INVENTIONS MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 24065-004 DIV
CURRENT APPLICATION NUMBER: US/09/679,729
CURRENT PILIG APPLICATION NUMBER: 09-01-0-04
PRIOR APPLICATION NUMBER: 09-277,457

PRIOR APPLICATION UMBER: 09-277,457
                                                                                                                                                                                                                                                                                                                      APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Sawada-Hirai, Ritsuko
APPLICANT: Barton, James C.
TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
FILE REFERENCE: 10653/002001
CURRENT APPLICATION NUMBER: US/09/277,457
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 17; DB 4; Length 17; 100.0%; Pred. No. 0.75;
US-09-503-444A-3

US-09-277-457-27

US-09-77-457-27

US-08-724-394A-21

US-08-724-394A-21

US-08-724-394A-21

US-09-252-991A-9942

US-09-252-991A-9942

US-09-252-991A-9141

US-09-252-991A-924

US-09-252-991A-924

US-09-252-991A-924

US-09-252-991A-924

US-09-252-991A-924

US-09-253-444A-2

US-09-503-444A-2

US-09-107-532A-3370

US-09-227-357-144

US-08-652-265-11
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                                                                                                                                                                                                                                                                               Sequence 30, Application US/09277457 Patent No. 6355425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: S65C Mutation US-09-277-457-30
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APPLICANT: Rothenberg, Barry E.
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Matches 17; Conserv
   RESULT 1
US-09-277-457-30
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US-09-679-729-30
   SEQ ID NO 30
LENGTH: 17
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Sequence 9808, Appl
Sequence 99, Appli
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Sequence 44,
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-652-265-44
US-08-834-497A-44
US-08-622-265-43
US-08-652-265-43
US-08-652-265-43
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US-08-652-265-3
US-08-634-497A-1
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                                                                                September 12, 2003, 23:34:04
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Maximum Match 100%
Listing first 45 summaries
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ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
CONTRAFE: FRASESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
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1155 Avenue of the Americas
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APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
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; Sequence 44, Application US/09503444A
; Patent No. 6228594
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ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, BITAN M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELERAX: 650-493-5556
TELERAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 44:
                      APPLICANT: Thomas, Winston J.
APPLICANT: Drayra, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Reder, John N.
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MOLECULE TYPE: DNA (genomic)
US-08-834-497A-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                               TITLE OF INVENTION: HE NUMBER OF SEQUENCES: 70 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
'..hog 17; Conservat
                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 Ave
CITY: New York
STATE: New York
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                  100.0%; Score 17; DB 4; Length 17; 100.0%; Pred. No. 0.75; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thomas, Winston J.
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Greder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Registary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIDH TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDRA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 576-0200
TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-1996
0.1: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/08652265 Patent No. 6025130 GENERAL INFORMATION:
                                                            OTHER INFORMATION: S65C Mutation US-09-679-729-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ATCATGAGTGTCGCCGT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                            1 ATCATGAGIGICGCGT 17
                                                                                                                                                                                                                                                                                                               1 ATCATGAGTGTCGCCGT 17
   ORGANISM: Artificial Sequence
                                                                                                                                                      Query Match 100.0
Best Local Similarity 100.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
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US-08-652-265-44
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                               FEATURE:
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APPLICANT: Drayna, Dennis T.
APPLICANT: Breder, John N.
APPLICANT: Gairke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: HERDITANT HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.6%; Score 15.4; DB 3; Length 32; Best Local Similarity 94.1%; Pred. No. 6.8; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                    SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: SMITH, WIlliam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
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STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43, Application US/08834497A; Patent No. 6140305
GENERAL INFORMATION:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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                                                                San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
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ZIP: 10036-2811
                                                                                                                           94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-834-497A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-652-265-43
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESEBE: Pennies: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Rederitary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-Feb-2000
CLASSIFICATION
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION NUMBER: 08/632,673
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %2-00-652-265-43
; Sequence 43, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-Apr-1996
ATTORNEY/ACENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28.462
REFERENCE/DOCKET NUMBER: 8907-
TELEPOMMURICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ATCATGAGTGTCGCCGT 26
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Gnirke, Andreas
APPLICANT: Tsucdy, David
APPLICANT: Tsuchinhashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMONICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                              8907-0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAX-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 41, Application US/08652265
; Patent No. 6025130
                          NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/POCKET NUMBER: 8907-
TELEPHONE: 212-790-9090
TELEPA: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ATCATGAGAGTCGCCGT 26
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-503-444A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic) US-08-652-265-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.6%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.6
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: TWO DRILL.
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Thomas
APPLICANT: Drayna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-652-265-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Breder, John N.
APPLICANT: Grirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
APPLICANT: Wolff, Roger K.
UNUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DCKET NUMBER: 8907-0056-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 661-41 PENNIE
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CIIY: New York STATE: New York
лек: US 08/632,673
16-APR-1996
N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
                                                                                                               APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/09503444A Patent No. 6228594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATCATGAGAGTCGCCGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCATGAGIGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-Apr-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.19
Matches 16; Conservative
                                APPLICATION NUMBER: UFILING DATE: 16-APR-1CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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US-09-503-444A-43
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16; Conservative

Matches

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Length 40;
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APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 15.4; DB 3; 94.1%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8907-0088-999
                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordberfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9808, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION NUMBER: 08/632,673
APPLICATION NUMBER: 08/630,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marc J. Rubenfield et al.
                                    Sequence 41, Application US/09503444A Patent No. 6228594 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect Versio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-Apr-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CAPRACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 212-869-9741
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Best Local Similarity 94.1
Matches 16; Conservative
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APPLICANT: MARC J.
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US-09-252-991A-9808/c
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TELERAX: 214
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RESULT 11
US-09-503-444A-41
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Galike, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTR: 10036-2011

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FLING DATE: 04-APP-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.6%; Score 15.4; DB 3; Best Local Similarity 94.1%; Pred. No. 7; Matches 16; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: CLASSIFICATION: NATURNEY/AGENT INFORMATION: NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION WOMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION S14
PRIOR APPLICATION 514
CLASSIFICATION 514
                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Pennie & Edmonds LLP
7: 1155 Avenue of the Americas
New York
New York
                                                                                                                                     Sequence 41, Application US/08834497A Patent No. 6140305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                             19 ATCATGAGAGTCGCCGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATCAIGAGIGICGCGF 17
  1 ATCATGAGTGTCGCCGT 17
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US-08-834-497A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                        US-08-834-497A-41
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90.6%; Score 15.4; DB 3; Length 1440; 94.1%; Pred. No. 12; ive 0; Mismatches 1; Indels 0;
                                         /phenotype= "normal or wild-type
(unaffected)"
/label= 24d2
                                                                                                                     FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d7
FEATURE:
                                                                                                                                                                                                                                                                                     NAME/KEY: allele

LOCATION: replace(1066, "g")

CTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"

CTHER INFORMATION: /label= 24d1

US-08-652-265-9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: SMITCH, Milliam M.
REGISTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10. Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Theder, John N.
APPLICANT: Greder, John N.
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                        LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotyg
OTHER INFORMATION: (unaffect
OTHER INFORMATION: /label= 2
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: sing]
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    allele
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILLE REFERENCE: 10/196/136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9808
LENGTH: 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREEF: Two Enbarcadero Center, Eighth Floor STRTY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.6%; Score 15.4; I
Best Local Similarity 94.1%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches
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NAME: Smith, William M.
REGISTRATION UNMBER: 30,223
REFERENCE/DOCKET UNMBER: 1795:
TELECOMMUNICATION INFORMATION:
TELEPANE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08652265 Patent No. 6025130
                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 ATCATGAGTGTCTCCGT 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222..1268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-652-265-9
                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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FEATURE.

NAME/KEY: CDS
LOCATION: 222.1268
FEATURE:
NAME/KEY: allele
NAME/KEY: allele
LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type
OTHER INFORMATION: /label= 24d2
FEATURE:
NAME/KEY: allele
LOCATION: replace(414, "a")
COCATION: replace(414, "a")
OTHER INFORMATION: /label= 24d7

OTHER INFORMATION: /label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: replace(1066, "g")
OTHER INFORMATION: '(phenotype= "normal or wild-type
OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.6%; Score 15.4; I
Best Local Similarity 94.1%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 13, 2003, 01:51:07 Job time : 4.06859 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATCATGAGTGTCGCCGT 17
  STRANDEDNESS: single
                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
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                                                                                                                                                                                                                                                           Gaps
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GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.

APPLICANT: Breder, John N.

APPLICANT: Breder, John N.

APPLICANT: Ruddy, David

APPLICANT: Tsuchhash, Zenta

APPLICANT: Tsuchhash, Zenta

APPLICANT: Wolff, David

CORRESPONDENCE ADDRESS: Bemonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: USA

COMMITY: USA

COMMITY: USA
                                                                                                                                                                                                                                                           0
                            DB 3; Length 1440;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
                                                                                                                                                                                                           90.6%; Score 15.4; Inlarity 94.1%; Pred. No. 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR SIGLATION: 314
PRIOR SIGLATION: 314
PRIOR APPLICATION NAMBER: US 08/652,265
FILING BATE: 23-MAX-1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-834-497A-9; Sequence 9, Application US/08834497A; Patent No. 6140305
                                                                                                                                                                                                                                                                                                                       406 ATCATGAGAGTCGCCGT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1440 base pairs
TYPE: nucleic acid
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CDS
222..1268
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Best Local Similarity
Matches 16; Conserv
                        LOCATION:
  NAME/KEY:
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Gaps

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Indels

1; DB 3;

Length 1440;

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77, Appl
INFORMA
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3864.876 Million cell updates/sec
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                                                                                                                                                          2003, 23:45:10 ; Search time 10.6787 Seconds
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Sequence 68,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.Seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NBW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NBW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-142-729-68
US-10-138-888-44
US-10-138-888-77
US-10-138-888-79
US-10-138-888-79
US-10-138-888-79
US-10-138-888-43
US-10-138-888-41
US-10-138-888-41
US-10-138-888-41
US-10-138-888-41
US-10-138-888-41
US-10-138-888-41
US-10-138-888-41
US-10-138-888-9
US-10-138-888-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1632420 segs, 1213878141 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                 1 atcatgagtgtcgccgt 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
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17
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Maximum DB
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Sequence 40, Appl
Sequence 42, Appl
Sequence 44, Appl
Sequence 64, Appl
Sequence 207, App
Sequence 207, App
Sequence 2087, App
Sequence 1944, App
Sequence 144, App
Sequence 144, App
Sequence 144, App
Sequence 337, App
Sequence 337, App
                          Sequence 27, Appl
Sequence 1, Appli
Sequence 107, Appli
Sequence 1076, Ap
Sequence 2356, Ap
Sequence 2356, Ap
                                                                    Appli
Appl
                                                                                                                                                                      Sequence 231, App
Sequence 124762,
Sequence 3444, Ap
Sequence 11, Appl
             GENERAL INFORMA
                     INFORMA
                                                                         Sequence 41, 1
Sequence 42, 1
Sequence 40, 1
                                                                    Sequence 1,
                     GENERAL
                                                                                                                             0.5-09-815-242-2087

0.5-09-983-965-5783

0.05-09-983-905-1944

1.05-09-983-802-144

1.05-09-988-802-144

1.05-09-988-805-331

1.05-09-128-676-331

1.05-10-027-632-124762

1.05-09-738-626-3444
US-09-981-606-1

US-10-138-888-1

US-10-138-888-3

US-09-981-606-27

US-10-301-844-2

US-10-301-844-2

US-09-974-301-1076

US-09-974-30-1076

US-09-974-30-1076

US-09-974-30-1076

US-09-974-30-1076

US-09-977-842-41

US-09-927-842-44

US-09-927-842-44

US-10-138-888-42

US-09-940-744-207

US-09-940-744-207

US-09-940-744-207

US-10-138-888-42

US-10-138-888-42

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US-10-138-888-42

US-10-142-729-64
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5982
10825
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ALIGNMENTS

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Gaps
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US-09-981-606-30
US-09-981-606-30
Sequence 30, Application US/09981606
Publication No. US20030129595A1
GENERAL INFORMATION:
APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders
FILER REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
PRIOR APPLICATION NUMBER: US/09/981,606
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN POR: 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 68, Application US/10142729; Publication No. US200301658881; GENERAL INFORMATION: APPLICANT: Brown, Bob D. APPLICANT: Riley, Timothy A.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: primer US-09-981-606-30
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US-10-142-729-68
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Sequence 62, Application US/10142729

Publication No. US20030165888A1

Sequence 62, Application US/10142729

Publication No. US20030165888A1

GENERAL INPORMATION:

APPLICANT: Broan, Bob D.

APPLICANT: Riley, Timothy A.

TITLE OF INVENTION: OLIGONOCLEOTIDE PROBES AND PRIMERS

TITLE OF INVENTION: OLIGONOCLEOTIDE PROBES FOR DIAGNOSTIC PURPOSES

FILE REFERENCE: OASBIO.005A

CURRENT APPLICATION NUMBER: US/10/142,729

PRIOR APPLICATION NUMBER: 60/306,229

PRIOR FILING DATE: 1298-08-18

PRIOR FILING DATE: 1998-08-18

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                  NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 17; DE Best Local Similarity 100.0%; Pred. No. 5.1 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 44: US-10-138-888-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) LOCATION: 1
; OTHER INFORMATION: n = modified base
US-10-142-729-62
                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 44:
                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/10138888; Publication No. US20030148972A1; GENERAL INFORMATION:
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            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ATCATGAGTGTCGCCGT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCATGAGTGTCGCCGT
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LENGIH: 39
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TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
FITE.OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
FILE REFERENCE: OASHIO: 005A
CURRENT TAPLICATION NUMBER: US/10/142,729
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/306,229
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 60/060,673
PRIOR APPLICATION NUMBER: 60/060,673
PRIOR APPLICATION NUMBER: 60/060,673
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 94
SOFTWARE: FASISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPBLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
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FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificial Oligonucleotide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1, 2
; OTHER INFORMATION: n = modified base
US-10-142-729-68
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Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44, Application US/10138888 Publication No. US20030148972A1 GENERAL INFORMATION: APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drayna, Dennis T.
Feder, John N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-138-888-44
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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LOCATION: replace(3878, "t")
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION:
TELEPAX: (212) 790-9090
TELEFAX: (212) 869-8864
OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing the 24d7 mutation" /note= "Hereditary Hemochromatosis (HH)gene 24d7 allele"
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             Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.
TILLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/10/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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SEQUENCE DESCRIPTION: SEQ ID NO: 79:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                   CONTER TOTAL
CONTER 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US20030165888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brian M. Poissant
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LOCATION: 5507.,6023
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LOCATION: 140..7319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATCATGAGTGTCGCCGT 17
                                                                                                                                            NUMBER OF SEQUENCES: 79
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brown, Bob D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
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COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IS Floppy disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PATENTON DATA:
APPLICATION NUMBER: US/10/138,888
FLOM CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497
Drayna, Dennis T.
Feder, John N.
Ghirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
WALIF, ROGER K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04 APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
FILING DATE: 04-APR-1996
FILING DATE: 04-APR-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 77:
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GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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222..1268
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATCATGAGIGTCGCCGT 17
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MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: USA
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US-10-138-888-79
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                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brown, Bob D. APPLICANT: Riley, Timothy A. TITLE OF INVENTION: OLIGONUCLECTIDE PROBES AND PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brian M. Poissant
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NATE: 05
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/652,655
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
APPLICATION NUMBER: US 08/630,912
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 43: US-10-138-888-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                   APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                     US-10-138-888-43
; Sequence 43, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/10142729
Publication No. US20030165888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 Wolff, Roger K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                   RESULT 9
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APPLICANT: Caplin, Brian
APPLICANT: Caplin, Brian
APPLICANT: Caplin, Brian
APPLICANT: Caplin, Brian
APPLICANT: Chen, Jian
APPLICANT: Saquence Analysis
FILE OF INVENTION: Sequence Analysis
FILE REPERENCE: 7475-67328
CURRENT APPLICATION NUMBER: US/09/927, 842
CURRENT APPLICATION NUMBER: US 60/224,726
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
## APPLICANT: Riley, Timothy A.
### TITLE OF INVENTION: OLIGONUCLEGIDE PROBES AND PRIMERS
### TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
### CURRENT APPLICATION NUMBER: US/10/142,729
### CURRENT APPLICATION NUMBER: US/10/142,729
### PRIOR PILING DATE: 2002-08-29
### PRIOR PILING DATE: 2001-07-18
### PRIOR FILING DATE: 1998-08-18
### PRIOR FILING DATE: 1997-10-02
### NUMBER OF SEQ ID NOS: 94
### NUMBER OF SEQ ID NOS: 94
### SOFTWARE: FastSEQ for Windows Version 4.0
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94.1%; Pred, No. 41;
1ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: n = modified base US-10-142-729-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/09927842 Publication No. US20030022177A1 GENERAL INFORMATION:
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Best Local Similarity 94.15
Matches 16; Conservative
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Best Local Similarity 94.11
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LOCATION: 1, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-927-842-43
                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 67
LENGTH: 21
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APPLICANT: RIJEY, TIMOCHY A.
TITLE OF INVENTION: OLIGONUCLECTIDE PROBES AND PRIMERS
TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
FILE REPRENDE: COASHO: O05A
CURRENT APPLICATION NUMBER: US/10/142,729
CURRENT APPLICATION NUMBER: 00/208-29
PRIOR APPLICATION NUMBER: 00/316,080
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 00/136,080
PRIOR FILING DATE: 1998-08-18
PRIOR FILING DATE: 1998-08-18
PRIOR PLING DATE: 1998-08-18
PRIOR FILING DATE: 1998-08-18
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                                                         REFERENCE/DOCKET NUMBER: 8907-095-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.6%; Score 15.4; I Best Local Similarity 94.1%; Pred. No. 42; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 15.4; D
94.1%; Pred. No. 42;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-138-888-41
                                  REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: n = modified base US-10-142-729-63
                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 206, Application US/09940244; Publication No. US20030044796A1; GENERAL INFORMATION: APPLICANT: Nerl, Bruce P. APPLICANT: Hall, Jeff G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 63, Application US/10142729; Publication No. US/20030165888A1; GENERAL INFORMATION; APPLICANT: Brown, Bob D.
                                                                                                                                                                                                   LENGIH: 40 base pairs
                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ATCATGAGAGTCGCCGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATCATGAGTGTCGCCGT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 ATCATGAGAGTCGCCGT
                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES FILE REFERENCE: OASBIO.005A
CURRENT APPLICATION NUMBER: 012/10/142,729
CURRENT FILING DATE: 2002-008-29
PRIOR FILING DATE: 2001-00-18
PRIOR FILING DATE: 2001-00-18
PRIOR FILING DATE: 1994-08-18
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 94
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/L0/138,888
FILING DATE: 02-May-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Artificial Oligonucleotide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/834,497 FILING DATE: 04-APR-1997 APPLICATION NUMBER: US 08/652,265 FILING DATE: 23-MAY-1996 APPLICATION NUMBER: US 08/632,673 FILING DATE: 16-APR-1996 APPLICATION NUMBER: US 08/630,912 FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%; Score 15.4; D
94.1%; Pred. No. 42;
Live 0; Mismatches
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Gnirke, Andreas
Ruddy, David
Tsuchihashi, Zenta
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Publication No. US20030148972A1
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APPLICANT: Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCATGAGTGTCGCCGT 17
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.69
Best Local Similarity 94.13
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-138-888-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER
                                                                                                                                                                                                                                                                                               SEQ ID NO 61
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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19 ATCATGAGAGTCGCCGT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nerl, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lukowizh, Andrew A.
TITLE OF INVENION: Methods and Compositions for Detecting Target Sequences
FILE REFERENCE: FORS-07459
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                  90.6%; Score 15.4; DB 11; Length 46; 94.1%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 46;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.6%; Score 15.4; DB 12; Best Local Similarity 94.1%; Pred. No. 42; Matches 16; Conservative 0; Mismatches 1;
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: Patentin version 3.1
SEQ ID NO 206
LENGTH: 46
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 206, Application US/10290386 Publication No. US20030152971A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    19 ATCATGAGAGTCGCCGT 35
                                                                                                                                                                                                                                                                                                               1 ATCAIGAGIGICGCCGI 17
                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                      FEATURE:
COTHER INFORMATION: Synthetic
US-09-940-244-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-10-290-386-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lyamichev, Victor
                                                                                                                                                                                                                                               Query Match 90.65
Best Local Similarity 94.15
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                       US-10-290-386-206
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LOCATION: replace(408, "c")
OTHER INFORMATION: /phenotype= "normal or wild-type (unaffected)"
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LOCATION: replace(414, "a")
OTHER INFORMATION: /phenotype= "normal or wild-type
(unaffected)"
                                                                                                         Feder, John N.
Galrke, Andreas
Ruddy, David
Tsuchiabahi, Zenta
Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/138,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-095-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
APPLICATION NUMBER: US 08/630,912
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 9, Application US/10138888
Publication No. US20030148972A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brian M. Poissant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 1440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 222..1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= 24d2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= 24d7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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FEATURE

1 ATCATGAGTGTCGCCGT 17

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0;
                                                                                                                                                               Query Match 90.6%; Score 15.4; DB 12; Length 1440; Best Local Similarity 94.1%; Pred. No. 54; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps
| NAME/KEY: allele | LOCATION: replace(1066, "q") | OTHER INFORMATION: /phenotype= "normal or wild-type | (unaffected)" | /label= 24dl | SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-10-138-888-9
                                                                                                                                                                                                                                                                                                                                                     Search completed: September 13, 2003, 01:57:07 Job time: 15.6787 secs
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Thu Feb 12 06:11:57 2004

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cgaactccalgggtttccagtagaatttcaagccagatgtggctgcagctgagtcagagtctgaaaggg
gggatcacatgttcaccgttgagtctctggactattatggaaaatcaaaccaacaagraagagtccacac
cctgcaggtcatcctgggctgtgaaattgcaaqaagacaacag accgagggctattggagtacgggta
gatgggcaggaccaccttgaattctgccctgacaacactggattggagagcagaaacccagggctggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtatgatgggfgttttttagcaggtaggaggcaaatatettgaaaggggttgtgaagagggtgttttteta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgaaaggetgtgeaetgeaegaatggaagageaeetgteeeagaaaaageateatggetatetgtgggtta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tottacaataattotatgagataggtactattatococatttotttttaaatgaagaaagtgaagtagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccgggcacggtggctcgcgctgtggtcccagggtgctgagattgcaggtgtgagccaccctgcccagcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tottotttaggoattaaattttagoaaagatatotoatotottottttaaaooattttotttttttgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttagaaaagttatgtagaaaaaagtaaatgtgatttacgctcattgtagaaaagctataaaatgaataca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgaagetttggggetacgtggatgaccagetgttegtgttetatgateatgagtgtegeegtgtggageee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccaccaagctggagtgggaaaggcacaagattcgggccaggcagaacagggcctacctggagagggactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgctgcgttcacactctctgcactacctcttcatgggtgcctcagagcaggaccttggtctttccttgt
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                                                        APPLICANT: Rothenberg et al.
TITLE OF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atgggcccgcgagccaggccggcgcttctcctcctgatgcttttgcagaccgcggtcct
Sequence 1, Application US/09981606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09981606-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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TITLE CF INVENTION: Mutations associated with iron disorders FILE REFERENCE: 24065-004CON
CURRENT APPLICATION NUMBER: US/09/981,606
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 09/277,457
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.1
LENGTH: 2506 Sequence 1, Application US/09981606 GENERAL INFORMATION: ORGANISM: Homo sapiens TYPE: DNA 09981606-1B